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GenCore version 5.1.6
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- protein search, using sw model OM protein December 14, 2004, 05:47:53 ; Search time 8.04852 Seconds (without alignments) 418.411 Million cell updates/sec Run on:

US-10-792-311-1

1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	scripti	outer membrane p	hypothetical prote	Tola protein PA097	outer membrane int	histone H1 - sea u	11-beta,	probable zuotin [i	histone H1 - sea u	probable NLP/P60 f	DNA topoisomerase	hypothetical prote	tolA protein - Esc	⊆	membrane spanning	DNA topoisomerase	histone H1-gamma,	kinetoplast-associ	histone H1 - Chlam	hypothetical prote	sperm tail-specifi	probable hupB - My	surface antigen A	hypothetical prote		histone H1-II - Vo	hypothetical prote		histone H1, gonada	H
SUMMARIES		! ! !																												
SUMIN	ID	4359	T03561	E83525	G64064	A25550	A28100	T50972	809388	T34625	JC6552	T34081	JV0057	F90725	G85576	G75403	A26721	A44937	859589	H96535	S51364	G70673	A60338	H59099	A32137	JN0748	T21503	A57591	HSUR1P	JN0747
	DB	. 7	7	7	~	~	7	7	7	7	7	7	7	~	~	7	~	ч	7	7	~	~	7	7	7	7	~	~	-	7
	Query Match Length		461	347	372	210	211	445	206	277	1015	1130	421	394	394	1021	217	1052	231	318	1390	214	1528	101	185	241	335	621	248	261
æ	Query Match		48.5	45.8	44.6	43.4	43.1	42.5	42.2	42.2	42.2	42.2	41.9	40.4	40.4	40.4	40.1	40.1	39.8	٩.	39.8	٩.	٩.	39.5	38.9	38.6	38.6	38.3	38.0	38.0
	Score	84	80.5	16	74	72	71.5	70.5	70	7.0	7.0	70	69.5	67	67	67	99	66.5	99	99	99	65.5	65.5	65	64.5	64	64	63.5	63	63
	Result No.	1	7	٣	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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Gaps

1;

Indels

48.5%; Score 80.5; DB 2; 60.0%; Pred. No. 0.25; ive 5; Mismatches 8;

Local Similarity 60.0 nes 21; Conservative

Query Match Best Local Si Matches 21;

1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35 ||: :|| ||| | ||||||: ||||||| :||| 30 AKEVVEKEAAAKDAAKEAKAR-EEAAAKDAAAKA 63

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Length 461;

hypothetical prote	hypothetical prote	probable erythrocy	histone H1 homolog	histone H1 (clone	penicillin-binding	histone H1 - rainb	histone H1 - midge	hypothetical prote	tolA protein [impo	zuotin-like protei	proton pump intera	penicillin-binding	translation initia	DNA topoisomerase	hypothetical prote
H96835	T49622	T09127	S61926	T06257	AD1683	HSTRIR	S40436	T10644	AG0592	T39683	T08942	AD1311	A82298	B87553	829309
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683	735	1701	182	288	826	206	244	266	376	442	628	827	868	899	217
0	0	0	7	7	۲.	m	m	m	m	m	m	'n	'n	'n	0
38	38	38	37	37	37	37	37	37	37	37.3	37	37	37	37	37
63	63	63	62.5	62.5	62.5	62	62	62	62	62	62	62	62	62	61.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Cispecies: Treponema phagedenis Cispecies: Treponema phagedenis Cispecies: Treponema phagedenis Cispecies: Treponema phagedenis Cispecies: 30-Jan-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
Ciscesion: B43592 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
Ciscesion: B43592 #sequence_revision 1891
A;Title: Treponema phagedenis encodes and expresses homologs of the Treponema pallidum Thay Reference number: A45592; MuID:91372983; PMID:1894368
A;Reference number: A45592; MuID:91372983; PMID:1894368
A;Reference number: DNA
A;Reference number: DNA
A;Residues: 1-384 < YEL>
A;Cross-references: UNIPROT:P29720; GB:M58563; NID:9155066; PIDN:AAA27480.1; PID:9155067
A;Note: the authors translated the codon TTC for residue 316 as Tyr, and CGA for residue C;Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein - Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03561
R;Vlcek, C.; Paces, V.; Malteev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003.
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003.
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003.
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003.
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003.
A;Ascession: T03561
A;Ascession: T03561
A;Ascession: T03561
A;Ascession: T03561
A;Ccoss-references: UNIPROT:O68124; EMBL:AF010496; NID:g3128256; FIDN:AAC16214.1; FID:g31
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAAK-KAYKKEAKAKAA-EAAAKEAAYEA 35
outer membrane protein TmpB - Treponema phagedenis
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A, Experimental source: strain PAO1 C, Genetics: A, Gene: tolA, PA0971

Local Similarity nes 23; Conserv

8

Query Match

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CiAccession: A25550
R;Knowles, J.A.; Childs, G.J.
Nucleic Acids Res. 14, 8121-8133, 1986
A;Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus and A;Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus and A;Reference number: A25550; MuID:87040778; PMID:3022245
A;Accession: A25550
A;Molecule type: DNA
A;Residues: 1-210 <KNO>
A;A;Residues: 1-210 <KNO>
A;Cross-references: UNIPROT:P06144; GB:X04488; NID:g9616; PIDN:CAA28177.1; PID:g9617
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004
C;Accession: A28100
C;Accession: A28100
Mol. Cell. Biol. 8, 1842-1844, 1988
A;Title: Characterization of the structure and transcriptional patterns of the gene encoc A;Reference number: A28100
A;Reference number: A28100
A;Accession: A28100
A;Accession: A28100
A;Accession: 1-211 cLAI>
A;Gessidues: 1-211 cLAI>
C;Superfamily: histone H1
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; embryo; nucleosome; nucleus
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R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000
A;Reference number: 225286
A;Accession: T50972
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-445 <SGH>
A;Cross-references: UNIPROT: Q9P3Q8; EMBL:AL389890; GSPDB:GN00116; NCSP:B24P7.270
A;Experimental source: BAC clone B24P7; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>"</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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N'Alternate names: protein B24P7.270
C.Species: Neurospora crassa
C.Species: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
histone H1 - sea urchin (Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 72; DB 2; Length 210;
Pred. No. 0.98;
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ilarity 66.7%; Pred. No. 1.1;
Conservative 2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 43.4%;
1 Similarity 59.0%;
23; Conservative 3
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Best Local Similarity
Matches 23; Conserva
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nes 20; Conserv
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A;Map position: 6
A;Introns: 98/3
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Best Local S:
Matches 20
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G64064
outenbrane integrity protein tolA - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Nug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: G64064; JG5212,
C;Accession: G64064; JG512,
M; Dis Scott, J; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.I.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Itle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: G64064
A;Accession: G64064
A;Status: nucleic acid sequence not shown; translation not shown
A;Holecule type: DNA
A;Residues: 1-372 < THGRS.
A;Accessidues: 1-372 < THGRS.
                                                            C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E83525
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Title: DNA
A;Status: preliminary
A;Status: preliminary
A;References: LNA
A;Residues: 1-347 <STO>
A;Cross-references: UNIPROT: P50600; GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG0436
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 'V', 2-47', A', 49-141,'R',143-164,'P',166-189,'R',191-202,'A',204-226,'A',228-
A;Cross-references: GB:U32470
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R;Sen, K.; Sikkema, D.J.; Murphy, T.F.
A;Title: 15-131, 1996
A;Title: Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA a A;Reference number: JC5212; MUID:97080550; PMID:8921895
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                                         Fold protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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A;Note: the authors translated the codon CGT for residue 190 as Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.8%; Score 76; DB 2; Length 347; ilarity 56.1%; Pred. No. 0.57; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.6%; Score 74; DB 2; Length 372; 58.1%; Pred. No. 0.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 AKKRAEDEAKKKAAEDAKKKAAEBAKKKAAEEAKKKAAAEA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAK---KEKAAKKAYKK---EAKAKAAEAAKEAAYEA 35
```

5 AKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35

5; Mismatches

Query Match Best Local Similarity 58.1 Matches 18; Conservative

C;Genetics: A;Gene: tolA A;Start codon: GTG

```
A,Title: cDNA cloning of Physarum polycephalum DNA topoisomerase I and expression analysi A,Reference number: JG6552; MUD:98245940; PMID:9583949
A,Accession. JG6552
A,Accession. JG6552
A,Molecule type: mRNA
A,Residues: 1-1015 <CZE>
A,CCSE>
A,CCSSE-references: UNIPROT:Q94705; GB:AF023910; GB:U63217; NID:g2642492; PIDN:AAC14193.1
A,Genetics:
A,Genetics:
A,Genetics:
A,Genetics:
C,Superfamily: eukaryotic type I DNA topoisomerase
C,Reywords: isomerase
F,974/Active site: Tyr #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein CO2F12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis
B;Miller, N.
Submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid CO2F12.
A;Reference number: Z21473
A;Reference number: Z21473
A;Reference number: Z21473
A;Reference number: Z21473
A;Residues: 1-1130 cMIL>
A;Residues: 1-1130 cMIL>
A;Residues: 1-1130 cMIL>
A;Residues: CESP:CO2F12.7
A;Residues: L118/1; 156/2; 239/2; 308/2; 398/1; 458/3; 591/1; 640/3; 756/2; 790/2; 8:
A;Introns: 11/2; 118/1; 156/2; 239/2; 308/2; 398/1; 458/3; 591/1; 640/3; 756/2; 790/2; 8:
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JV0057; Webster, R.E.
J; Bacteriol. 171, 6600-6609, 1889
A;Title: Nucleotide sequences of the tolA and tolB genes and localization of their produc
A;Reference number: JV0057; MUID:9078104; PMID:2687247
A;Accession: JV0057
A;Accession: JV0057
A;Accession: JV0057
A;Residues: 1-421 clrV
A;Residues: 1-421 clrV
A;Residues: 1-421 clrV
A;Residues: UNIPROT:P19934; GB:M28232; NID:g148018; PIDN:AAA24683.1; PID:g148019
A;Residues: Bcance: Strain JM105
A;Rose: Louis Muller of the initiation codon GTG for residue 1 as Val
A; Rose, D.J; Mau, B.; Shao, Y.
Science 277, 1455-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Attle: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                          Score 70; DB 2; Length 1015;
Pred. No. 5.9;
6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 70; DB 2; Length 1130;
Pred. No. 6.4;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KKYAKKEKAAKKAYKKE------AKAKAAEAAAKEAAY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 KKEKAAKKAYKKEAKAKA-----AEAAKEAAYE
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 42.9%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.2%;
Best Local Similarity 51.4%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Parechinus angulosus (angulate urchin)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S09388
R;Hill: C.S.; Martin, S.R.; Thomas, J.O.
EMBO J. 8, 2591-2599, 1989
A;Title: A stable alpha-helical element in the carboxy-terminal domain of free and chromaly. Reference number: S09388; MUID:90060019; PMID:2583125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9XAQ3; EMBL:AL078618; PIDN:CAB44532.1; GSPDB:GN00070; SCOEL A;Experimental source: strain A3(2) C;Genetics: A;Genetics: A,Gene: SCOEDB:SC10A7.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable NLP/P60 family secreted protein - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: O5-Nov-1999 #sequence_revision O5-Nov-1999 #text_change O9-Jul-2004 C; Accession: T14625 #sequence_revision 05-Nov-1999 #text_change O9-Jul-2004 R; Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M. submitted to the EMBL Data Library, June 1999 #; Reference number: Z21549 #; A; Reference number: Z21549 A; A; Accession: T134625 A; Status: preliminary; translated from GB/EMBL/DDBJ #; Molecule type: DNA.
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JC6552
DNA topoisomerase (EC 5.99.1.2) - slime mold (Physarum polycephalum)
NyAlternate names: emega-protein; micking-closing enzyme; type I DNA topoisomerase
C;Species: Physarum polycephalum
C;Species: DS-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: JC6552
R;Czerwinski, R.M., Lipniacki, A.; Staron, K.
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                                         Length 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70; DB 2; Length 277;
Pred. No. 2;
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                               DB 2;
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                                      Score 70.5; Di
Pred. No. 2.6;
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                                                                                                                                                                                                                                                                                                                                                                          urchin (Parechinus angulosus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/Status: preliminary
A/Molecule type: protein
A/Residues: 1.206 eHIL>
A/Cross-references: UNIPROT:Q7M409
C/Superfamily: histone HI
C/Keywords: chromosomal protein
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Best Local Similarity 54.3%;
Matches 19; Conservative
                                  ch 42.5%;
l Similarity 57.1%;
20; Conservative
                         Query Match
Best Local Similarity
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histone H1 - sea
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922 ASKTAPKKAAAKPAAKKAAPKKAASKSAKTPAAKA 956
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Job time : 10.0485 secs
22; Conservative
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es 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary A; Molecule type: DNA
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Best Local &
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Matches
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(885576

membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C; Accession: (88576
R; Perna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamcusis, K.; Apodaca, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Date: 18-Jul-2001
R;Accession: F90725
R;Assunaga, N.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res: 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q8X965; GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: tolA
           A;Cross-references: GB:AB000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960; A;Experimental source: strain K-12, substrain MG1655 C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t G;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Geneticos: A;Geneticos: A;Geneticos: A;Geneticos: GF A;Asp position: 17 min A;Start codon: GTG
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Pred. No. 5.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
                                                                                                                                                                                                                   Cikeywords: nucleotide binding; P-loop; transmembrane protein R;14-34/Domain: transmembrane #status predicted <MSS> F;78-301/Domain: helical #status predicted <HSR> F;78-362/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KYAKKEKAAKKA----YKKEAKAKAAEAAKEAAYEA 35
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Pred. No. 3.2;
4; Mismatches
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Best Local Similarity 52.6%;
Matches 20; Conservative
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Best Local Similarity
Matches 22; Conserv
  A;Residues: 1-421 <BLAT>
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Best Local Similarity
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A, Status: preliminary
A, Molecule type: DNA
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A;Molecule type: DNA
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C.; Mal
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A;Cross-references: UNIPROT:Q9RULO; GB:AE001983; GB:AE000513; NID:g6459123; PIDN:AAF1094:
A;Experimental source: strain R1
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RA;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
7
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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Gaps
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                                                                            1 AKKYAKKE--KAAKKAYKK-----EAKAKAAEAAAKEAAYEA 35
8; Indels
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                                                                                                                                                                                                                                   DNA topoisomerase I - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 1
C;Superfamily: bacterial type I DNA topoisomerase
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illarity 51.4%; Pred. No. 12;
Conservative 3; Mismatches
Mismatches
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REPEAT
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08t9r3 leishmania
08t9r3 leishmania
08t073 thodopseudo
06d7f3 erwinia car
06n8x8 rhodopseudo
02a27215 rhodopseudo
07tu15 synechococc
001395 drosophila
0937k4 erwinia chr
P50600 pseudomonas
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Caf05892 neurospor
Q8myc2 mytilus chi
P44678 haemophilus
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P06144 lytechinus
Q88rd8 pseudomonas
Q89jl2 bradyrhizob
Q9zhc5 mycobacteri
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Cae50058 corynebac
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O68124 rhodobacter
Q89da0 bradyrhizob
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Q6mc2 bdellovibri
Cae79230 bdellovib
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P62228 corynebacte
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                                                                                         December 14, 2004, 05:47:53 ; Search time 39.2827 Seconds (without alignments) 512.646 Million cell updates/sec
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5.1.6
Compugen Ltd
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                                                                                                                                                                                                                                                                      1825181 segs, 575374646 residues
version 9
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WST3_DROHY

0937K4

TOLA_PSEAE

095AX2

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CAF05892

CAF058
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CAE16_CORD1
CAE50058
Q9WWI1
Q08N16
Q08124
Q08124
Q08124
Q89DA0
Q8WQ44
Q85DR3
Q6MT9R3
Q6MT9R3
Q6MT9R3
Q6MT9R3
CAE28621
Q6MT9R3
CAE28621
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Maximum Match 100%
Listing first 45 summaries
                                                             protein search, using sw model
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DBH_MYCSM
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Gapop 10.0 , Gapext 0.5
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GenCore (c) 1993
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Match Length DB
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Maximum DB
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
          Q7qc14 anopheles g
Q8fp30 corynebacte
Q8fp30 corynebacte
Q7w473 pseudomonas
Q6f298 mesoplasma
Q87v67 pseudomonas
Q71ny2 lactobacill
Q71iy2 lactobacill
Aq06605 lactobaci
Q9p3d8 neurospora
Q9p3d8 neurospora
                                                                                                                                                              streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                  Yelton D.B., Limberger R.J., Curci K., Malinosky-Rummell F., Sliviensky L., Schouls L.M., van Embden J.D.A., Charon N.W.; "Treponema phagedenis encodes and expresses homologs of the Treponema pallidum TmpA and TmpB proteins."; pallidum TmpA and TmpB proteins."; Infect. Immun. 59:3685-3691(1991).

-!- FUNCTION: Tmp may serve as a porin or transport protein for large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treponemal membrane protein B.
17 X 5 AA tandem repeats of K-A-A-[AKR]-
[ED].
                                                                                                                                                                                                                                                                                                                                                         Bacteria; Špirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBL_TaxID=162;
                                                                                                                                                           Q9xaq3
                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Treponemal membrane protein B precursor (Antigen tmpB).
Treponema phagedenis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Outer membrane-associated
                                                                                                                                                                                                                                                             384 AA
                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; B43592; B43592.
InterPro; IPR008941; TPR-like.
Antigen; Outer membrane; Repeat; Signal.
                     RS16_COREF
                                                                                               Q711Y2
AAQ06805
Q9P3Q8
Q7YSZ7
Q7M409
Q9XAQ3
                                              Q7W477
Q6F298
Q87V67
Q7UMV5
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                                  087X39
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1-2.
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1-9.
1-10.
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MEDLINE=91372983; PubMed=1894368;
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  00000000000000
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151
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RESULT 3
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1-15.
1-16.
1-17.
6 X 8 AA tandem repeats of [EA]-A-A-R-X-
A-A-E.
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MEDLINE=22965443; PubMed=14602910;
MEDLINE=22965443; PubMed=14602910;
MEDLINE=22965443; PubMed=14602910;
Cacdeno-Tarxaga A.-M., Efstratiou A., Dover L.G., Holden M.T.G., Pallen M.J., Bentley S.D., Berara G.S., Churcher C.M., James K.D., De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T., Rablinowitch E., Rutherford K.M., Thomson N.R., Unwin L., Whitehead S., Barrell B.G., Parkhill J.;
Whitehead S., Sarrell B.G., Parkhill J., Sarrell J., Sa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 82; DB 1; Length 157; Pred. No. 0.34;
                                                                                                                                                                                                                                                                                       50.6%; Score 84; DB 1; Length 384; 64.9%; Pred. No. 0.47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
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157 AA; 16985 MW; BB3FC04EEAD9708A CRC64;
                                                                                                                                                                                                                                                     6E94CBC74294DE8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEKAAK-KAYKKEAKAKAA-EAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Name=rpsP; OrderedLocusNames=DIP1532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 AA.
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PROSITE; PS00732; RIBOSOMAL_S16; FALSE_NEG.
Complete proteome; Ribosomal protein.
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5; Mismatches
                                                                                                                                       2-1.
2-2.
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2-5.
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                                                                                                                                                                                                                                                     42677 MW;
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les 24; Conservative
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Best Local Similarity
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RS16_CORDI
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"The Pseudomonas putida peptidoglycan-associated outer membrane
lipoprotein (PAL) is involved in maintenance of the integrity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Biotype gravis / NCTC 13129;
MEDLINE-22965443; PubMed=14602910;
Cerdeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A.,
Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,
Whitehead S., Barrell B.G., Parkhill J.;
"The complete genome sequence and analysis of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96422022; PubMed=8824639;
Rodriguez-Herva J.J., Ramos J.;
"Characterization of an OprL mull mutant of Pseudomonas putida.";
J. Bacteriol. 178:5836-5840(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
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                                                                                                                                                                                                                                                                                         Bacieria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=1717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.4%; Score 82; DB 2; Length 157; 64.5%; Pred. No. 0.34; tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 AA; 16985 MW; BB3FC04EEAD9708A CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                           Last sequence update)
Last annotation update)
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EMBL, BX248358; CAE50058.1; --.
Ribosomal protein.
                                                                       Created)
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PRT;
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Bacteriol. 178:1699-1706(1996)
                                                           02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                             Corynebacterium diphtheriae
                                                                                                                                                                              30S ribosomal protein S16. RPSP OR DIP1532.
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
CAE50058
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Gaps

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48.8%; Score 81; DB 2; Length 372; 56.1%; Pred. No. 0.94; ive 3; Mismatches 9; Indels
                                                                                                     372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
                                                        PRINTS; PRO0624; HISTONEHS.
TIGREPAMS; TICR01352; tonB_Cterm; 1.
Complete proteome.
SEQUENCE 372 AA; 40133 MW; 87F4
                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=SB1003;
MEDLINE=97404404; PubMed=9256491;
InterPro; IPR005819; Histone_H5.
InterPro; IPR010528; TolA.
InterPro; IPR006260; TonB_C.
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                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 60.0
21; Conservative
                                                                                                                                                               23; Conservative
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                                           Pfam; PF06519; TolA; 1
                                                                                                                                                   Similarity
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Matches
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GO:0000786; C:nucleosome; IEA.
GO:0000863; C:nucleosome; IEA.
GO:000864; C:nucleosome; EAA.
GO:0003087; E:DNA binding; IEA.
GO:000865; F:protein transporter activity; IEA.
GO:0008334; P:nucleosome assembly; IEA.
GO:0015031; P:protein transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22433060; PubMed=12534463; Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Brita dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Hollmes M., Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F., Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M., Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K., Moazez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Elsen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                    Rodriguac Herva J.J.;

Rodriguac Herva J.J.;

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

R BEBLI X74218; CAB50780.1; -.

R GO; GO:0016020; C:membrane; IEA.

GO; GO:000786; C:mucleosome, IEA.

GO; GO:0005634; C:mucleosome, IEA.

GO; GO:0005634; C:mucleosome assembly; IEA.

GO; GO:0008565; F:protein transporter activity; IEA.

GO; GO:0008565; F:protein transporter activity; IEA.

R GO; GO:0008565; F:protein transporter activity; IEA.

R GO; GO:0015031; P:protein transporter activity; IEA.

R GO; GO:0015031; P:protein transporter activity; IEA.

R GO; GO:0015031; P:protein transporter activity; IEA.

R InterPro; IPR00589; GO]A.

R InterPro; IPR00589; GO]A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002). HBL; AE016778; AAN66845.1; -. HSSP; P50600; LLRO. TIGR; PP1221; -.
   Ramos-Gonzalez I.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0624; HISTONEHS.
TIGREAMS; TIGRO1352; tonB Cterm; 1.
SEQUENCE 372 AA; 40133 WW; 87P49785ECC3COBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 AKKKAEDEAKKKAEEEAKKAAABEAKKKAAEDAKKKAAEEA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYA-----KKEKAAKKAYKKBAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Biopolymer transport protein TolA.
Name=tolA; OrderedLocusNames=PP1221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 AA
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                                             SEQUENCE FROM N.A. STRAIN=mt-2;
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EMBL, AF010496; AAC16214.1; -.
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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Hypothetical protein.
SEQUENCE 461 AA; 49516 MW; DD8DA03418BC0368 CRC64;
                                                160 AKKKAEDEAKKKAEEEAKKAAAEEAKKKAAEDAKKKAAEEA 200
1 AKKYA-----KKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
Rhodobacter capsulatus (Rhodopseudomonas capsulata)
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Last annotation update)
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Matches

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RESULT Q8WQ44

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SEQUENCE FROM N.A.
STRAIR=CGA009 / ATCC BAA-98;
PubMed=14704707; DOI=10.1038/nbt923;
PubMed=14704707; DOI=10.1038/nbt923;
Laximer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L. Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C., Harrison F.H., Gibson J., Harwood C.S., "Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";
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STRAIN=CGAOO9 / ATCC BAA-98;
PubMed-4704707;
Larimer F.W., Chain P., Hauser L., Lamerdin J., Malfatti S., Do
Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; DB 2; Length 105; 0.56;
                                                                                                                                                       Length 111;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
                                                                                                                                                                                                         Indels
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                                                                                                     16168F3B54960E83 CRC64;
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SEQUENCE 105 AA; 11042 MW; CEDBS9B3D937E980 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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                                                                                                                                               Score 79.5; DB 2;
Pred. No. 0.46;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                    76 AKKVAKKPAKKAAKKPAKKPAK-KAAKKAA 108
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GO; GO:0006334; P:nucleosome assembly; IEA.
InterPro; IPR005819; Histone H5.
PRINTS; PR00624; HISTONEH5.
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Pred. No. 0.
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EMBL; BX572603; CAE28621.1; -.
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                                                                                                     111 AA; 11162 MW;
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Best Local Similarity 67.6%;
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhodopseudomonas palustris.
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nes 24; Conservative
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05-JUL-2004
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CAE28621;
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Q6N503;
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Papageorgiou F.T., Soteriadou K.P.,
Papageorgiou F.T., Soteriadou F.P.,
Papageorgiou F.T., Soteriadou F.T.,
Papageorgiou F.T
                                                                                                                                                                                                                                   Gaps
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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCBI_TaxID=5664;
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5671;
"Complete genomic sequence of nitrogen-fixing symbiotic bacterium
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                                                                                                                                                                         48.2%; Score 80; DB 2; Length 117; 56.8%; Pred. No. 0.43;
                                                                                                                                                                                                                             8; Indels
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; A4469106; AAL76335.1; -.
GO; GO:00005634; C:nucleosome; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005677; F:DNA binding; IEA.
                                                                                                                        117 AA; 11800 MW; 1DC651CC17A1F2B5 CRC64;
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Last sequence update)
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Last annotation update)
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Pred. No. 0.41;
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                    Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; APO05962; BAC52804.1; -.
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
18 kDa nuclear protein.
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Nuclear protein.
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Name=lnp18;
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7

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Matches

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Harrison F.H., Gibson J., Harwood C.S., Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";
                                                                     Nat. Biotechnol. 22:55-61(2004).
-!- SIMILARITY: Belongs to the ompA family.
-!- SIMILARITY: Belongs to the ompA family.
-!- SIMILARITY: Belongs to the ompA family.
GO: 00106021; C:integral to membrane; IEA.
GO: GO:0005741; C:mitcohondrial outer membrane; IEA.
GO: GO: 0015289; F:porin activity; IEA.
InterPro: IPR006664; Bac OmpA.
InterPro: IPR006665; OmpĀ/MotB.
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CAE27215;
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Holeva M.C., Thomson N.R., Bentley S.D., Churcher C., Mungall K.,
Atkin K., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Barrell B.G., Parkhill J., Toth I.K.,
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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Pubbled=14704707; DOI=10.1038/mbt923;
Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
                                                                                                                                                                                                                                                                   Gaps
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  Torres y Torres J.L., Peres C.,
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pectobacterium.
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Bradyrhizobiaceae, Rhodopseudomonas.
NCBI_TaxID=1076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 47.0%; Score 78; DB 2; Length 395; 1 Similarity 57.1%; Pred. No. 2.1; 20; Conservative 4; Mismatches 11: Thele
Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Harrison F.H., Gibson J., Harwood C.S.; "Complete genome sequence of the metabolically versatile
                                                                                                                                                                                                                                                              7; Indels
                                                                  photosynthetic bacterium Rhodopseudomonas palustris.";
Nat. Biotechnol. 22:55-61 (2004).
EMBL, Bx572603; CAE28621.1; -.
Hypothetical protein.
SEQUENCE 105 AA; 11042 MW; CEDBS9B3D937B980 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
OmpA/MotB domain, possible porin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                               47.3%; Score 78.5; DB 63.2%; Pred. No. 0.56;
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                                                                                                                                                                                                                                                              24; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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QGNBXB;
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Nat. Biotechnol. 22:55-61(2004).

EMBL, BX572598, CAE27215.1;
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Bradyrhizobiaceae, Rhodopseudomonas.
                                                                                                                                                                                                         Query Match 47.0%; Score 78; DB 2; Length 441; Best Local Similarity 57.1%; Pred. No. 2.3; Matches 20; Conservative 4; Mismatches 11; Indels
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                                                                                                                                                 441 AA; 44811 MW; F6BB66A4AFE183A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 441 AA; 44811 MW; F6BB66A4AFE183A0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                    259 AKEVAAKEAAAKAAAEAAAKQAAADEAAKKAADEA 293
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RS16_SYNPX
ID RS16_SYNPX
AC O7TUU5;
DT 05-UUL-2004 (Rel. 44, Last sequence update)
DT 05-UUL-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    441 AA
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02-MAR-2004 (TrEMBLrel. 27, Last seq
02-MAR-2004 (TrEMBLrel. 27, Last ann
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                                                          ProDom; PD000930; OmpA/MotB; 1.
Complete proteome; Porin; Signal.
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STRAIN=CGA009 / ATCC BAA-98;
PubMed=14704707;
Pfam; PF00691; OmpA; 1.
PRINTS; PR01021; OMPADOMAIN.
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                                                                                               SEQUENCE FROM N.A.

MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
Chain P., Lamerdin J.B., Regala W., Allen B.E., McCarren J.,
Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
"The genome of a motile marine Synechococcus.";
Nature 424:1037-1042(2003).
--- SIMILARITY: Belongs to the S16P family of ribosomal proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches 10; Indels
                   Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=84588;
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InterPro; IPR000307; Ribosomal S16;
Pfam; PF00886; Ribosomal S16; 1.
ProDom; P0003791; Ribosomal S16; 1.
TICRFAMS; TIGR0002; S16; 1.
Complete Proteome; Ribosomal Protein.
SEQUENCE 140 AA; 15194 MW; 99C48AE8
Name=rpsP; OrderedLocusNames=SYNW1617;
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December 14, 2004, 05:47:53 ; Search time 38.692 Seconds (without alignments) 324.499 Million cell updates/sec Run on:

US-10-792-311-1 166 Title: Perfect score:

1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_23Sep04:* 1: geneseqp1980s:* geneseqp1980s:* Database

geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:* geneseqp2000s:* geneseqp2002s:* geneseqp2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

	Description	Aay82571 Copolymer	Aay82572 Copolymer		_		-	-	-	Adp99051 C. albica	Abu26064 Protein e	Abu40185 Protein e	Aar06445 Recombina	Abu38313 Protein e	Abj18771 Pseudomon	Abo80835 Pseudomon	Abg71044 Tumour ne		Abo23507 Haemophil	Aab08170 Peptide m	Adel0657 Structura	Adel0656 Structura	Adel0606 Structura	Adel0607 Structura	Adk15676 Library f	Adk15675 Library f
OFFICE	ΙD	AAY82571	AAY82572	AAY82576	AAY82574	AAY82577	AAY82573	AAY82575	AAG70868	ADP99051	ABU26064	ABU40185	AAR06445	ABU38313	ABJ18771	ABO80835	ABG71044	ABG80418	AB023507	AAB08170	ADE10657	ADE10656	ADE10606	ADE10607	ADK15676	ADK15675
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	Query Match Length	35	45	98	99	109	26	77	427	427	157	372	154	347	347	407	80	372	372	40	80	80	80	80	80	80
de	Query Match	100.0	65.1	65.1	63.6	63.3	63.0	63.0	52.1	52.1	49.4	48.8	45.8	45.8	45.8	45.8	44.9	44.6	44.6	44.3	43.4	43.4	43.4	43.4	43.4	43.4
	Score	166	108	108	105.5	105	104.5	104.5	86.5	86.5	82	81	16	16	9/	9/	74.5	74	74	73.5	72	72	72	72	72	72
	Result No.		7	m	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Adk15626 Nucleatin Ade10608 Structura Ade10658 Structura Adk15677 Library f Aby5546 Bifdobac Abu39775 Protein e Adm11701 Peptide 1 Aar06446 Recombina Abu42038 Protein e Adm1301 Peptide 1 Aar0646 Recombina Abu42038 Protein e Adm25508 Human pro Aagg1997 C glutami Abu28559 Protein e Abb62028 Drosophil Aar910180 Polycatio	
ADK15626 ADK15625 ADE10608 ADE10658 ADK15627 ADK15627 ABN11701 ABN11701 AAN001997 AAM2508 AAM2508 AAM2508 AAM2508	AAB08168 AAR90181 AAW06688
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ALIGNMENTS

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1. AAY82571 standard; peptide; 35 AA. (first entry) 28-JUL-2000

Unidentified.

WO200018794-A1.

06-APR-2000.

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; Gad A,

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention of escribes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

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of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune baemolytic anaemia, autoimmune cophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Gilllain-Barrés syndrome, Hashimoto's disease, idiopathic mysodema, mysethenia gravis, syndrome, Hashimoto's disease, idiopathic mysodema, mysethenia gravis, psoriasis, pemphigus vulgatis, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, colypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer accetate molecules, which
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pemphigus vulgaris; systemic lupus erythematosus.
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Best Local Similarity 100.C
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular

Claim 10; Page 14; 72pp; English

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

(YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

WPI; 2000-317499/27.

Gad A, Lis D;

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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP) which has an identified molecular weight and an an among an identified molecular weight and an an actid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer of the invention are used as molecular weight markers for glatiramer of the invention are used as molecular weight markers for glatiramer contracting and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, autoimmune hamolytic anaemia, autoimmune carbitis, autoimmune thrombocytopaenia purpura, collitis, contact sensitivity disease, dispetes mellitus, Garves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, graft-versus-bost disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glatifamer acctate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; dulllain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
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                                                                                                                                                                                                                                                                                                                                                                                                          properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 108; DB 3; Lengtn 40, Pred, No. 1.4e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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(TEVA-) TEVA PHARM USA INC.
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Best Local Similarity 64.4%
Local Similarity 64.4%
Local 29, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 45 AA;
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Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4. AAY82574 standard; peptide; 66 AA Claim 10; Page 14; 72pp; English. 99WO-US022402. 98US-0101693P. 28-JUL-2000 (first entry) 1 AKKYAKKEKAAKKAY-Sequence 86 AA; WO200018794-A1. 25-SEP-1998; 24-SEP-1999; 36-APR-2000. AAY82574; Query Match Matches AAY82574

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related terrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroidmine haemolytic anaemia, autoimmune cophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxodedma, mysthania gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, and delayed-type hypersensitivity. The properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
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Match 65.1%; Score 108; DB 3; Length 86; Local Similarity 57.4%; Pred. No. 2.8e-05; es 27; Conservative 2; Mismatches 6; Indels 12; -----KKEAKAKAAEAAKEAAYEA 35

Gaps

40 AKKYAKAAKAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAKEAAYEA 86

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyrodi, antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

(YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Gad A, Lis D;

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight and an offer composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer cof the invention are used as molecular weight markers for glatiramer cof the invention are used as molecular weight markers for glatiramer cactate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune tharoidmine haemolytic anaemia, autoimmune thyroidmitis, autoimmune thrombocytopaenia purpura, colitis, contact compositivity disease, disease, idiopathic mysoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, chronic immune haemolymic mysoedema, myasthenia gravit, or graft-versus-host disease, and delayed-type hypersensitivity. The correct co
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                                                                Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
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                                                                                                                                                                   Claim 10; Page 14; 72pp; English.
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AAY82577 standard; peptide; 109 AA. 61 EAAYEA 66 AAY82577 셤

28-JUL-2000 (first entry) AAY82577;

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.

WO200018794-A1. Unidentified

pemphigus vulgaris; systemic lupus erythematosus

99WO-US022402. 24-SEP-1999;

06-APR-2000.

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides [1] for determining the molecular weight invention describes polypeptides [1] for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer actactate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroidmits, autoimmune veorestinitis, crohn's cliease, chronic immune thyroidmits, autoimmune veorestinitis, crohn's cliease, chronic immune thyroidmits, graves disease, Guillain-Barre's syndrome, Hashinoto's disease, idopathic mysoedema, myashinota graves, capaciasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graff disease, copypertides of the invention have defined molecular weights and physical properties which are analogous to glatiramer accetate molecules, which makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                 Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                                                                                                                                                                                               Claim 10; Page 14; 72pp; English
                                                                    (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                       98US-0101693P.
                                                                                                                                                                                                    WPI; 2000-317499/27.
                                                                                                                                                  Gad A, Lis D;
                       25-SEP-1998;
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Sequence 109 AA;

Gaps 10; / Match 63.3%; Score 105; DB 3; Length 109; Local Similarity 62.2%; Pred. No. 7.9e-05; Anishatches 5; Indels 1 65 AKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKAAKEAAYEA 109 1 AKKYAKKEKAAKKAY----KKEA----KAKAAEAAKEAAYEA 35 Query Match Matches ઢ 원

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AAY82573 standard; peptide; 56 AA. RESULT 6

AAY82573;

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteogathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crown's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified

WO200018794-A1

pemphigus vulgaris; systemic lupus erythematosus.

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer acteate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases of treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases Such diseases include arthritic conditions, autoimmune cophoritis, autoimmune thyroidmine haemolytic anaemia, autoimmune cophoritis, autoimmune thyroidmine haemolytic anaemia, autoimmune cophoritis, autoimmune thyroidmine, e.g. multiple sclerosis, from structus arthritis, osteoarthritis, autoimmune baemolytic anaemia, autoimmune cophoritis, autoimmune thyroidmine, e.g. multiple sclerosis, fornic arthritis, autoimmune thyroidmine, e.g. multiple sclerosis, fornic confict in autoimmune thyroidmine in a school of the school of the invention in the cophorities with the sease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myrosedema, myasthenia gravis, psirdraced diseases which an be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The properties which are analogous to glatizamer acetate molecules, which makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                                                                                                  Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
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51.8%; Pred. No. 4.6e-05;
tive 4; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Page 14; 72pp; English.
                                                                                                                                                              (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                     99WO-US022402.
                                                                                                                 98US-0101693P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 56 AA;
                                                                                                                                                                                                                                      Lis D;
                                                                  24-SEP-1999;
                                                                                                                 25-SEP-1998;
                        06-APR-2000.
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                                                                                                                                                                                                                                      Gad A,
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Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteogathic; immunosupressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; ornouic immune thrombocytopaemia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5. 1 AKKYAKKEKA----AKKAYKK------EAKAKAAEAAKEAAYEA 35 AAY82575 standard; peptide; 77 AA. (first entry) 28-JUL-2000 AAY82575; RESULT 7 **AAY82575**

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The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemia and neurodegeneration. The present sequence is one of the C. albicans proteins of the invention
                                                                                                                                                                                                                                                                                                                                    Yeast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diploid fungal cell; allele; gene disruption cassette; promoter replacement fragment; antifungal; fungicide; gene therapy; infection; Candida albicans.
                                                                                                                                                                                                Luyten WHML, Malcorps IKL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C. albicans specific gene, orf19.2709, protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.1%; Score 86.5; DB 4;
65.7%; Pred. No. 0.044;
ive 3; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 KEKAKKEKAAKKWEKESGSRKAAEEAAAKKAAEEA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KKYAKKEKAAKKAYKKEAKAKAA-EAAAKEAAYEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP99051 standard; protein; 427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 24; Fig 2; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boone C,
                                                               03-JUL-2000; 2000WO-BE000077.
                                                                                                            99EP-00870141
                                                                                                                                                                                              De Backer MD,
Reekmans RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-2003; 2003WO-US040618.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 65...
Best Local 23; Conservative
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ELITRA CANADA LTD
                                                                                                                                                      (JANC ) JANSSEN PHARM NV
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                                                                                                                                                                                                                                                                    WPI; 2001-367042/38.
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                                                                                                                                                                                                                                                                                                                                                                                                          certain diseases.
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                                                                                                                                                                                                                                                                                          N-PSDB; AAH29904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 427 AA;
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                                                                                                                                                                                                   Contreras RH,
                                                                                                            01-JUL-1999;
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                       11-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determaining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glattramer cof the invention are used as molecular weight markers for glattramer cactate related terrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases continued activated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, contract coophoritis, autoimmune thyroidmune theomory topaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic mysocedema, myasthenia gravis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, colypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which correct conditions are subjected at markers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.0%; Score 104.5; DB 3; Length 77; 65.8%; Pred. No. 6.4e-05; live 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKEKAAKKAY---KKEAKAKAAEAAAKEAAYEA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C albicans apoptosis associated protein #48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG70868 standard; protein; 427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 14; 72pp; English
                                                                                                                                                      99WO-US022402.
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                                                                                                                                                                                                                                             (YEDA ) YEDA RES & DEV CO L'
(TEVA-) TEVA PHARM USA INC.
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                                                               WO200018794-A1.
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                                                                                                                                                                                                                                                                                                               Gad A, Lis D;
                     Unidentified.
                                                                                                                                                      24-SEP-1999;
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                                                                                                         06-APR-2000
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Matches

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RESULT

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Gaps

1;

Indels

DB 4; Length 427;

Constructing a strain of diploid fungal cells in which both alleles of a gene are modified comprises modifying the alleles of a gene in the fungal cells by recombination using a gene disruption cassette and a promoter replacement fragment

Claim 44; SEQ ID NO 7226; 163pp; English.

The invention relates to a novel method for constructing a strain of dipold fungal seels in which he allelse of a gene as modified. The method comprises medifying the allelse of a gene as modified. The method comprises medifying the allelse of a gene as modified. The method comprises medified in the method comprises assembling a conjecture of Exploid fungal cells according to the process of a gene as a prometra of the process of the gene a conjecture and the process of the gene and the process of a fightoid fungal at the collection; a nucleic acid molecules where substantially all the different genes that is essential to the cultarion of the survival or a fungal and the different genes that is essential to the cultarion of a fungal seem to a target mucleic acid molecules of a fungal, that contributes to the virulence of a diploid fungat to an artifungal agent; identifying an antifungal seem of a diploid fungal to a target mucleic despendent of a fungal agent; identifying an antifungal agent for treatment of a mammalian disease, corralating changes in the constraing a process of a diploid fungal to a target molecule comprising a process of process of process of a diploid fungal to a purified to the nucleic acid molecule comprising an uncleance endoding a gene product comprising a product conference of a diploid fungal to a long the product of comparising of at least of constants of an artification (Appsprised some process of a purified to a gene transf at least one amino acid sequence selected from ADP98826-ADP99135; a method assisted by a computer for identifying a putatively essential gene of a fungus; and a protein array comprising proteins, where at least one protein comprises an amino acid sequence or a portion of an amino acid sequence selected from ADP98516-ADP98825. The novel methods and compositions have fungicide activity. The compositions amy be used in gene therapy. The composition and methods are useful for drug screening purposes or for diagnosing, preventing or treating infections associated

ä the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense autisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) with Candida albicans. These may also be used for constructing strains useful for identification and validation of gene products as effective targets for therapeutic intervention, for identifying and validating gene products as effective targets for therapeutic intervention, and for collecting identified essential genes. This sequence represents the protein of a Candida albicans fungal specific gene of the invention.

NOTE: This sequence was downloaded from an electronic sequence listing provided on the WIPO website. New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. The invention relates to an isolated nucleic acid comprising any one of Antisense; prokaryotic essential gene; cell proliferation; drug design. Gaps Zyskind JW; Xu HH; ij 52.1%; Score 86.5; DB 8; Length 427; 65.7%; Pred. No. 0.044; ive 3; Mismatches 8; Indels Ohlsen KL, Forsyth RA, Protein encoded by Prokaryotic essential gene #11591. 283 KEKAKKEKAAKKWEKESGSRKAAEEAAAKKAAEEA 317 2 KKYAKKEKAAKKAYKKEAKAKAA-EAAAKEAAYEA 35 Haselbeck R, Yamamoto R, Claim 25; SEQ ID NO 53988; 1766pp; English. ABU26064 standard; protein; 157 AA Malone C, Carr GJ, 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 21-MAR-2002; 2002WO-US009107 06-MAR-2002; 2002US-0362699P Corynebacterium diphtheriae, Malone (first entry) 23; Conservative (ELIT-) ELITRA PHARM INC. Zamudio C, Trawick JD, Query Match Best Local Similarity WPI; 2003-029926/02. N-PSDB; ACA29934. Sequence 427 AA; WO200277183-A2 19-JUN-2003 03-OCT-2002. ABU26064; υŗ Wang | Matches 8888888888888ઠ

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identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, s activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of trains; or (13) identifying the target of a compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational cup discovery programs, or for screening homologous nucleic acids required for cellular proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this capter did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the target prokaryotic_sequences

Etp.wipo.int/pub/published_pct_sequences
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the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein encoded by Prokaryotic essential gene #25712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.4%; Score 82; DB 6; 64.5%; Pred. No. 0.054; ative 3; Mismatches
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 KKKAKEEAAAKAAAEAEAAAKAEEAPAEEAA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KKYAKKEKAAKKAYKKEAKAKAAEAAAKEAA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID NO 68109; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU40185 standard; protein; 372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-03022859.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2002; 2002WO-US009107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 64.5
Hes 20; Conservative
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-029926/02.
N-PSDB; ACA44055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 157 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200277183-A2
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Wall
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ID ABU40185

ID ABU4

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concoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated encoding a polypeptide whose expression is inhibited by the antisense polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation or the activity of agene in an operon required for proliferation or that has an activity against a bhological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed, (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for ceilular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing genes encoding random polymers of aminoacid(s) - for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 48.8%; Score 81; DB 6; Length 372; Best Local Similarity 56.1%; Pred. No. 0.17; Matches 23; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant copolymer 1-77, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 AKKKAEDEAKKKAEEEAKKAAAEEAKKKAAEDAKKKAAEEA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYA----KKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR06445 standard; protein; 154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89US-00312541.
90US-00473845.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1990-255848/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 372 AA;
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03-JAN-1991
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for improve the expression of rCOP-1 polypeptides in B. coli, genes coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 Us4691009), MRLL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences, originating from the Co-1 long between the Protein A and rCOP-1 sequences, originating from the control and protein. TWOP-1-77 contains oligonucleotide duplexes incoding the following segments: YKK, EAE, KAK, AAK, and AAA. The N-terminal alanine residue is left behind following CMST cleavage of the fusion protein. The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain amino acids. See also AAQ05665. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        screening
recombinant polypeptide(s) with biological and/or immunological activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 76; DB 2; Length 154;
Pred. No. 0.26;
4; Mismatches 9; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #23840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 KKKAKEAERAKKAKKYKKYKKEAEAAKAAKAAAAAYK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KKYAKKEKAAKKA----YKKEAKAKAAEAAKEAAYE 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 66237; 1766pp; English.
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                                  Disclosure; Fig 11; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU38313 standard; protein; 347
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Carr GJ,
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25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                  45.8%;
54.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Conservative
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-029926/02
N-PSDB; ACA42183.
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  Sequence 154 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Wall D,
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The invention relates to an isolated nucleic acid comprising any one

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coffee nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

encoding a polypeptide whose expression is inhibited by the antisense

mucleic acid; (2) a host cell containing the vector; (3) an isolated

contisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide or its fragment whose expression is inhibited by the

contisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibited by the

proliferation or the activity of a gene in an operon required for

proliferation or that has an activity against a biological pathway or

continued for proliferation, or that inhibits cellular proliferation; (8)

conquired for proliferation, or that inhibits cellular proliferation of an identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a

compound; activity; (11) a culture comprising strains in which the extent or compound activity; (11) a culture compound that inhibits proliferation of an organism acts; or 13) identifying the target of a compound that inhibits the

compound; or the strains is present in a culture or collection of the which each of the strains is present in a culture or collection of correctly proliferation of an organism. The antisense nucleic acids required contiferation of an organism. The antisense moleic acids required contiferation of an organism or some captide are useful for dentifying proteins or screening for homologous nucleic acids required for dentifying proteins or screening for homologous mucleic acids required for dentifying proteins or screening to a compound acids required for dentifying proteins or screening to a compound acids required for dentifying proteins or screening to a compound acids required for dentifying proteins or screening to a compound acids required for dentifying proteins or screening to a compound acids required for dent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed patent bublished pot_sequences
  the 6213 antisense sequences given in the specification where expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biofilm formation modulation; biofilm-associated disease; cystic fibrosis; AIDS; middle ear infection; acne; periodontal disease; catheter-associated infection; medical device-associated infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.8%; Score 76; DB 6; Length 347; 56.1%; Pred. No. 0.6; ive 5; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABJ18771 standard; protein; 347 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-APR-2001; 2001US-0285190P.
24-OCT-2001; 2001US-0344142P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-APR-2002; 2002WO-US012532.
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(HARD ) HARVARD COLLEGE.
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Best Local Similarity 56.1.
These 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bangera MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-075601/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2002.
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The invention comprises a method for identifying a compound capable of modulating biofilm formation by bacteria. The method of the invention is useful for identifying a compound capable of modulating biofilm formation by bacteria or modulating bacterial antibiotic resistance. The method of the invention is also useful for diagnosing and treating a subject (especially an immunocompromised human) that is afflicted with a biofilm-sasociated disease or disorder, such as: oystic fibrosis; AIDS; middle ear infections; acne; periodontal disease; catheter-associated infections; and medical device-associated infections. The present amino acid sequence represents a protein that is used in the invention
                                   Identifying compound capable of modulating biofilm formation by bacteria/bacterial antibiotic resistance, useful for treatment of biofilm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
                                                                                                                                                                                                                                                                                                                                                                           45.8%; Score 76; DB 6; Length 347; 56.1%; Pred. No. 0.6; ative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAK---KEKAAKKAYKK---EAKAKAABAAAKBAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 29581; 455pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa polypeptide #13010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deloughery
                                                                                                          Claim 1; Page 119-120; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABO80835 standard; protein; 407 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00252991.
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                                                                                                                                                                                                                                                                                                                                                                                          Local Similaricy
hes 23; Conservative
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                                                                     associated disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABD14406
 N-PSDB; ABT14593
                                                                                                                                                                                                                                                                                                                                            Sequence 347 AA;
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including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences AB067826-sequence represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                           Gaps
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1 Similarity 56.1%; Pred. No. 0.7;
23; Conservative 5; Mismatches 7; Indels
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                                                                                                                                                                            seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                          Sequence 407 AA;
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Search completed: December 14, 2004, 06:01:08 Job time : 46.692 secs

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us-10-792-311-1.rapb

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December 14, 2004, 05:52:22; Search time 86.8354 Seconds (without alignments) 143.965 Million cell updates/sec
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| cgn2 6/ptodata/1/pubpaa/USO7_PUBCOMB.ppp:*
| cgn2 6/ptodata/1/pubpaa/USO6_NEW_PUB.ppp:*
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| cgn2 6/ptodata/1/pubpaa/USO6_PUBCOMB.ppp:*
| cgn2 6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp:*
| cgn2 6/ptodata/1/pubpaa/USO8_NEW_PUB.ppp:*
| cgn2 6/ptodata/1/pubpaa/USO8_NEW_PUB.ppp:*
| cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
| cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
| cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
| cgn2 6/ptodata/1/pubpaa/USO9_PUBCOMB.ppp:*
| cgn2 6/ptodata/1/pubpaa/USO9_NEW_PUB.ppp:*
| cgn2 6/ptodata/1/pubpaa/USO9_PUBCOMB.ppp:*
| cgn2 6/ptodata/1/pubpaa/USO10_PUBCOMB.ppp:*
| cgn2 6/ptodata/1/pubpaa/USO10_PUBCOMB.ppp:*
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| cgn2 6/ptodata/1/
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1585576 segs, 357178320 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                   OM protein - protein search, using sw model
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seq length: 200000000
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Perfect score:
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Maximum DB E
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

COTTON

			Description	Sequence 1, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 7, Appli	Sequence 3, Appli	Sequence 5, Appli	Sequence 53988, A	Sequence 68109, A	Sequence 120, App	Sequence 66237, A	Seguence 8, Appli	Sequence 16, Appl
SOMMAKIES			ID	US-09-816-989A-1	US-09-816-989A-2	US-09-816-989A-6	US-09-816-989A-4	US-09-816-989A-7	US-09-816-989A-3	US-09-816-989A-5	US-10-282-122A-53988	US-10-282-122A-68109	US-10-127-032-120	US-10-282-122A-66237	US-09-820-843A-8	US-10-467-421-16
			DB	6	σ	σ	σ	σ	σ	σ	15	15	14	15	10	16
			Length	35	45	86	99	109	26	77	157	372	347	347	372	372
	æ	Query	Match Length DB 1	100.0	65.1	65.1	63.6	63.3	63.0	63.0	49.4	48.8	45.8	45.8	44.6	44.6
			Score	166	108	108	105.5	105	104.5	104.5	82	81	92	9/	74	74
		Result	No.	-	7	m	4	2	9	7	80	6	10	11	12	13

RESULT

Sequence 13, Appl Sequence 14, Appl Sequence 64, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 675, Appl Sequence 6751, Appl Sequence 6751, Appl Sequence 6751, Appl Sequence 6751, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 100, Appl Sequence 20, Appl Sequence 203, Appl	Sequence 65.2, A Sequence 16, Appl Sequence 16, Appl Sequence 61735, A Sequence 27, Appl
US-10-177-725-13 US-10-177-725-14 US-10-177-725-64 US-10-177-725-64 US-10-393-449-13 US-10-393-449-64 US-10-393-449-64 US-10-393-449-64 US-10-393-449-64 US-10-177-725-65 US-10-177-725-65 US-10-393-449-15 US-10-393-449-15 US-10-282-122A-6992 US-10-282-122A-6992 US-10-282-122A-6992 US-10-296-115-1023 US-10-296-115-1023 US-10-296-115-1023 US-10-296-115-1023 US-10-296-115-1023 US-10-393-449-20 US-10-393-449-20 US-10-393-449-20 US-10-393-449-20 US-10-393-449-20 US-10-393-449-20 US-10-393-449-20 US-10-393-449-20 US-10-369-115-27374 US-10-369-115-27374	US-10-282-122A-65262 US-10-177-725-16 US-10-393-449-16 US-10-282-122A-61735 US-10-229-567-27
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4 0 0 0 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 4 4 4 4 1 5 6 4 6

ALIGNMENTS

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APPLICANT: dad. Alexander
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: 2609/6001-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 1001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1
LENGTH: 35
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100.0%; Pred. No. 1.8e-11;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-816-989A-1
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Matches 3
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APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 1998-09-25
PRIOR PILING DATE: 1998-09-25
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Doria
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
CURRENT APPLICATION NUMBER: US/09/816, 989A
CURRENT FILING DATE: 1998-09-25
PRIOR PPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.6%; Score 105.5; DB 9; Length 66; 43.9%; Pred. No. 0.00014; tive 2; Mismatches 4; Indels 3
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Best Local Similarity 62.2%; Pred. No. 0.00027;
Matches 28; Conservative 2; Mismatches 5; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 43.99
Matches 29; Conservative
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     GENERAL INFORMATION:
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US-09-816-989A-3
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                 Sequence 2, Application US/09816989A

Patent No. US20020115103A1

ABREAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: Lis, Doris

TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

TITLE OF INVENTION: COPOLYMER: US/09/816,989A

FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT PILING DATE: 1998-09-25

PRIOR FILING DATE: 1998-09-25

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1
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Patent No. US20020115103A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lis, Doris

TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT PILING DATE: 1998-09-25

PRIOR FILING DATE: 1998-09-25

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.1%; Score 108; DB 9; Length 45; Best Local Similarity 64.4%; Pred. No. 5.2e-05; Matches 29; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
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Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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US-09-816-989A-2
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LENGTH: 86
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LENGTH: 45
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TITLE OP INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
  Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
                                                                                                         Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 64.5
Matches 20; Conservative
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Sequence 5, Application US/0981698A

Sequence 5, Application US/0981698A

Sequence 5, Application US/0981698A

GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYBEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION NUMBER: US/09/816,989A

CURRENT APPLICATION NUMBER: US/0101,693

PRIOR FILING DATE: 1998-09-25

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PATCHIL VERSION 3.1
                                                                              APPLICANT: Lis, DOTIS

TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 06/101,693
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3
LENGTH: 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.0%; Score 104.5; DB 9; Length 56; Best Local Similarity 51.8%; Pred. No. 0.00016; Matches 29; Conservative 4; Mismatches 2; Indels 2:
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; Sequence 53988, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence PEATURE:
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
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US-10-282-122A-6623
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Matches
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                     PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-19-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR
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| Sequence 120, Application US/10127032
| Publication No. US2003011374241
| GENERAL INFORMATION:
| APPLICANT: Whiteley, Marvin
| APPLICANT: Bangera, M. Gita
| APPLICANT: Greenberg, Everett Peter
| TITLE OF INVENTION: BIOFILM FORMATION
| TITLE OF INVENTION: BIOFILM FORMATION
| FILE REFERENCE: UIZ-070CP
| CURRENT APPLICATION NUMBER: US/10/127,032
| CURRENT APPLICATION NUMBER: US 60/285,190
| PRIOR APPLICATION NUMBER: US 60/285,190
| PRIOR FILING DATE: 2001-04-20
| PRIOR SPELICATION NUMBER: US 60/344,142
| NUMBER OF SEQ ID NOS: 170
| SOFTWARE: FastSEQ for Windows Version 4.0
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llarity 56.1%; Pred. No. 0.42;
Conservative 3; Mismatches 9; Indels
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Best Local Similarity 56.1%; Pred. No. 1.4;
Matches 23; Conservative 5; Mismatches 7; Indels
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Matches 23; Conserv
CURRENT FILING DATE:
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SEQ ID NO 120
LENGTH: 347
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JABLEANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATCHIN version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR PRINK APPLICATION NUMBER: 60/191,078
PRIOR PELIGATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PELION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-23
PRIOR PELING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Porsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 45.8%; Score 76; DB 15; Length 347; Local Similarity 56.1%; Pred. No. 1.4; 14; Indels 18; Conservative 5; Mismatches 7; Indels
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
Sequence 66237, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                   APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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FULLIAGE OF SECTION NO. USECULOSTICATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Beele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT PELING DATE: 1099-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR PAPLICATION NUMBER: US 09/169,015
PRIOR PAPLICATION NUMBER: US 09/169,015
PRIOR PELING DATE: 1998-10-08
PRIOR PELING DATE: 1998-10-08
PRIOR PELING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR PELING DATE: 1998-10-08
PRIOR PELING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
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Pred. No. 0.82;
3; Mismatches 9; Indels
                                                                                                                                                                                                              Score 72; DB 14; Length 80;
Pred. No. 0.82;
3; Mismatches 9; Indels
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US-10-177-725-14
Sequence 14, Application US/1017725
; Publication No. US20030143562A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial sequence
                                                   TYPE: PRT ORGANISM: Artificial sequence
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Best Local Similarity 60.0%;
Matches 18; Conservative
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Best Local Similarity 60.0%;
Matches 18; Conservative
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                                                                                                                                    OTHER INFORMATION: synthetic US-10-177-725-13
SEQ ID NO 13
LENGTH: 80
                                                                                                             FEATURE:
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APPLICANT: Begenberger, Jakob M.
APPLICANT: Peelle, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT PILE REPERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/17, 725
CURRENT PILING DATE: 1090-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR RAPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
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44.6%; Score 74; DB 16; Length 372;
Best Local Similarity 58.1%; Pred. No. 2.4;
Matches 18; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                  44.6%; Score 74; DB 10; Length 372;
58.1%; Pred. No. 2.4;
tive 5; Mismatches 8; Indels
                                                                                                                                 NAME/KEY: misc_feature

CTHER INFORMATION: outer membrane integrity protein (tolA)

NAME/KEY: misc_feature

CTHER INFORMATION: gi|1573353

US-09-820-843A-8
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Sequence 16, Application US/10467421
Publication No. US20040116665A1
GENERAL INFORMATION:
APPLICANT: Berthet, Francois-Kavier Jacques
APPLICANT: Denoel, Philippe
APPLICANT: Poolman, Jan
APPLICANT: Thonnard, Jan
APPLICANT: Thonnard, Joelle
TITLE OF INVERTION: Vaccine Composition
FILE REFERENCE: B42259
CURRENT APPLICATION NUMBER: US/10/467,421
CURRENT FILING DATE: 2003-08-08
FRIOR APPLICATION NUMBER: PCT/EP02/01361
FRIOR APPLICATION NUMBER: PCT/EP02/01361
FRIOR APPLICATION NUMBER: CON-08-08
FRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 98
NUMBER OF SEQ ID NOS: 98
SEQ TWARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Haemophilus influenzae US-10-467-421-16
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Best Local Similarity 58.19
Matches 18, Conservative
                                                      TYPE: PRT ORGANISM: H. influenzae
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US-10-177-725-13
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SEQ ID NO 8
LENGTH: 372
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Sequence Seq

54,

Sequence Sequence

Sequence Sequence Sequence

Sequence:

Run on:

Searched:

Database

Result

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APPLICANT: ADMINISTRANCE AND DEVELORMENT CO., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REPERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 45
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DESCRIPTIOE
US-09-405-743A-2
                                                                                                                                                                                                                                                                                                                                  Seguence 1, Application US/09405743A
Seguence 1, Application US/09405743A
Patent No. 6514338
GENERAL INFORMATION:
APPLICANT: Yead Research and Development Co., Ltd.
APPLICANT: Yead Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT PELICAL NUMBER: US/09/405,743A
CURRENT PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
EROGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-1
US-09-248-796A-20228
US-08-152-488-11
US-08-152-488-11
US-08-303-025-13
US-08-303-025-13
US-08-677-304-10
US-08-677-304-11
US-08-436-7038-3
US-08-436-7038-3
US-08-436-7038-15
US-08-436-7038-15
US-08-929-414-1
US-08-929-651-1
US-08-929-651-1
US-08-93-674-51
US-08-93-674-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 100.0%; Score 166; DB 4; Local Similarity 100.0%; Pred. No. 2.8e-13; tes 35; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
    US-09-405-743A-1
  Query Match
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Matches
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Sequence 2, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 18922, A
Sequence 18922, A
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 16, Appl
Sequence 16, Appli
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Sequence 201, App
Sequence 201, App
Sequence 204, Ap
Sequence 21, Appl
Sequence 3802, Ap
Sequence 3802, Appl
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26989, A
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27, Appl
                                                                                             December 14, 2004, 05:47:53 ; Search time 9.82067 Seconds (without alignments) 236.351 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-405-743A-6

US-09-405-743A-6

US-09-405-743A-7

US-09-405-743A-3

US-09-405-743A-3

US-09-405-743A-3

US-09-405-743A-3

US-09-405-743A-3

US-09-228-991A-29581

US-08-152-488-13

US-08-152-488-13

US-08-303-025-15

US-08-303-025-15

US-08-303-025-16

US-08-303-025-16

US-09-303-038-4

US-09-436-703B-4

US-09-417-264-27

US-09-417-264-27

US-09-489-034-13565

US-09-205-426-201

US-09-205-426-201

US-09-107-532A-5044

US-09-1107-532A-5094

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US-09-114-132
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                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
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                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 200000000
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166
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Match Length
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Perfect score:
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Patent No. 6514938

GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION:
GENERAL ERFERENCE:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/405,743A

CURRENT APPLICATION NUMBER: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1
                                        Sequence 7, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL TITLE OF INVESTIGATION GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
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Patent No. 6514938
GENERAL INFORMATION:
APPLICANT Yeda and Development Co., Ltd.
APPLICANTON:
GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 104.5; DB 4; Length 56;
Pred. No. 7.8e-06;
4; Mismatches 2; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAAKKAY----KKEA----KAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.3%; Score 105; DB 4;
62.2%; Pred. No. 1.4e-05;
iive 2; Mismatches 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKA----AKKAYKK-----
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 51.8%;
Matches 29; Conservative
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Matches 28; Conservative
    RESULT 5
US-09-405-743A-7
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US-09-405-743A-3
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                                                                                                                                                                                                                                                                 SEQ ID NO 7
LENGTH: 109
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LENGTH: 56
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                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                          RESULT 3
US-09-405-743A-6
Sequence 6, Application US/09405743A
Sequence 6, Application US/09405743A
Sequence 6, Application US/09405743A
Settle No. 6514938
GENERAL INFORMATION:
APPLICAMT: Yeak Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 6
LENGTH: 86
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-405-743A-4

is Sequence 4, Application US/09405743A

is Patent No. 651438

is GRENERAL INFORMATION:

APPLICANT: Yeak Research and Development Co., Ltd.

is TITLE OF INVENTION:

FILLE REFERENCE: 60807-A

is CURRENT APPLICATION NUMBER: US/09/405,743A

is CURRENT PILING DATE: 1999-09-24

is NUMBER OF SEQ ID NOS: 7

is SOFTWARE: Patentin Ver. 2.1

is SEQ ID NO 4

i. LENGTH: 66
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                                                  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKEKAAKKAY-----KKEAKAKAAEAAKEAAYEA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 108; DB 4; Length 86; Pred. No. 4.7e-06; 2; Mismatches 6; Indels
65.1%; Score 108; DB 4; Length 45; 64.4%; Pred. No. 2.4e-06; ive 1; Mismatches 5; Indels
                                                                                                                      1 AKKYAKKEKA--AKKAYK----KEAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: CTHER INFORMATION: PEPTIDE US-09-405-743A-6
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OTHER INFORMATION: PEPTIDE
US-09-405-743A-4
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Best Local Similarity 57.4%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
  Query Match
Best Local Similarity 64.44
Matches 29; Conservative
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Best Local Similarity 43.9
Matches 29; Conservative
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  7; Indels
                                                                                                                                                                                                                                                                 APPLICANT: Wakefield, Thomas W.
APPLICANT: Wakefield, Thomas W.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEB: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranicord
STRATE: New Jersey
COUNTRY: United States of America
                                                                         215 AKKRAEDEAKKKAAEDAKKKAAEDAKKKAAEEAKKKAAAEA 255
                                              1 AKKYAK---KEKAAKKAYKK---EAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DGS
SOFTWARE: WordPerfect 6; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: S14
PRIOR PAPLICATION: WOMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INPORMATION:
NAME: ROHM, Benita J
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 28,664
TELEPHONE: 908-276-3344
TELEPHONE: 908-276-344
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  Mismatches
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DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
                                                                                                                                                               RESULT 10
US-08-152-488-13
; Sequence 13, Application US/08152488
; Patent No. 5534619
; GENERAL INFORMATION:
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  23; Conservative
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PUBLICATION INFORMATION:
AUTHORS: N/A
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Matches 19; Conserva
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STRANDEDNESS: N/
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US-08-303-025-15
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  Matches
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT PILING DATE: 1999-02-12
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 407
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                                                                                                                                                                                                           Query Match 63.0%; Score 104.5; DB 4; Length 77; Best Local Similarity 65.8%; Pred. No. 1.1e-05; Matches 25; Conservative 4; Mismatches 6; Indels
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                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: PEPTIDE
US-09-405-743A-5
                                                                                                                                                                                                                                                                                                                                           40 AKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKEAAYEA 77
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; Sequence 18922, Application US/09248796A
; Patent No. 6747137
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18922
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Best Local Similarity
Matches 23; Conserv
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Best Local Similarity
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SEQ ID NO 5
LENGIH: 77
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Patent No. 5919761
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
                                                                                     CITY: Crafford
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07016-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARRE: WordPerfect 6; ASCII (DOS) Text
CURENT APPLICATION NUMBER: US/08/677,304
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                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INPORMATION:
NAME: Rohm, Benita J.
REGISTATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 28,664
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: No. 5721212 Relevant
TOPOLOGY: No. 5721212 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 6601 Woodward Avenue
STREET: Suite 1525
CITY: Detroit
                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 61.3
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide ORIGINAL SOURCE:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-08-436-703B-2
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40.7%; Score 67.5; DB 1; Length 32;
Best Local Similarity 61.3%; Pred. No. 0.097;
Matches 19; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08677304
Patent No. 5721212
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL
                                     GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
                                                                                                                                                                                                                                                                                                                  CITY: Detroid
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: IBM PC compatible
OPERATING STATE: MS-DOS v.6.22
SOFTWARE: WORDPERFECT 6.1; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SERT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
TELEPHONEY AGENT INFORMATION:
TELEPHONES: 313-496-8454
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGRIH: 32 amino acids
words.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
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                                                                                                                                                                                                                                                                Est Benita J, Rohm, Esq.
150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      )
DOCUMENT NUMBER: PCT/US92/08069
;
FILING DATE: 14-AUG-1993
US-08-303-025-15
Sequence 15, Application US/08303025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-08-677-304-13
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à g us-10-792-311-1.rai

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Benita J, Rohm, Esq.
STREET: 661 Woodward Avenue
CLASSIFICATION: 514

PRIOR APPLICATION DATA
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REFERENCE/DOCKET NUMBER: 7WH-060548-00231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-496-7622
TELEPHONE: 313-496-8454
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYRE: amino acid
TYRE: AMINO acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Detroit
STATE: Michigan
COUNTRY: Detroit
A8226
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: MOST (1008) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FLING DATE: 08-MAY-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: N/A
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , TITLE: N/A;
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-436-703B-4; Sequence 4, Application US/08436703B; Patent No. 5919761
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ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 32;
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---- 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-303-025-16

| Sequence 16, Application US/08303025
| Patent No. 5614494
| Patent No. 5614404
| APPLICANT: Wakefield, Thomas W. APPLICANT: AAPLICANT: Stanley, James C. TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 16
| CORRESPONDENCE ADDRESS: ADDRESSEE Benita J, Rohm, Esq. STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Detroit
STATE: Michigan
COUNTY: United States of America
ZIP: 48226-4415
COMPUTER READABLE FORM:
MBDION TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS v.6.22
SOFTWARE: WordPerfect 6.1; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
40.7%; Score 67.5; DB 2;
Best Local Similarity 61.3%; Pred. No. 0.097;
Matches 19; Conservative 2; Mismatches 9;
                                              COUNTY: United States of America
ZIP: 48226
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: Propy disk 1.44Mb, 3.5"
COMPUTER: PROPY disk 1.44Mb, 3.5"
COMPUTER: PROPY DEAD STATEM: MS-DOS
SOFTWARE: MordPerfect 6;
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATYORNEY/AGENT INFORMATION:
NAME: ROMM, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WK-060548-00233
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313.965-1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AKKAAKKAKKAKKAAKKAAKKAAKKAKK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
  STATE: Michigan
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 313-965-1951
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-436-703B-2
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g

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1;
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REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WK-060548-00233
TELECOMONICATION INFORMATION:
TELEPHONE: 313-965-1956
TELEPHONE: 313-965-1951
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acide
TYPE: ANANDENESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
MUTHORS: N/A
TITLE: N/A
TITLE: N/A
US-08-436-7038-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

Search completed: December 14, 2004, 05:50:15 Job time : 10.9635 secs

g

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                    Copyright
```

- protein search, using sw model OM protein December 14, 2004, 05:47:53 ; Search time 10.3481 Seconds (without alignments) 418.411 Million cell updates/sec Run on:

US-10-792-311-2

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 2 K 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	L L	membrane spanning	membrane spanning	tolA protein - Esc	hypothetical prote		sperm tail-specifi	histone H1-beta, e	probable hupB - My	DNA topoisomerase	outer membrane pro	hypothetical prote	mst101-1 protein -	TolA protein PA097	histone H1 homolog	histone H1, gonada	1-acylglycerol-3-p	asparaginyl-trna s	hypothetical prote	probable NLP/P60 f	probable zuotin (i	probable DNA topoi	1		hypothetical prote	a	hypothetical prote	cgcr-1 protein - C	histone H1 - midge
SUMMARIES	ID	· `	F90725	G85576							B87553			S34153	E83525	S61926	HSUR1P									•	A26721 .			S40436
	EQ 1		•		•	•	7						~	••	~		-		~		•	7								7
	Query Match Length		394	394	421	239	243	1390	211	214	895	384	195	344	347	187	248	262	298	311	277	445	952	194	206	291	217	62	200	246
do	Query	48.6	46.0	46.0	46.0	44.4	42.3	42.3	42.0	42.0	41.3	40.6	40.4	40.4	40.4	39.9	38.5	38.5	38.5	38.3	37.8	37.8	37.8	37.6	37.6	37.6	37.3	37.1	37.1	37.1
	Score	٠.	98	98	96	94.5	90	σ	89.5	89.5	88	86.5	98	98	86	82	82	82	82	81.5	80.5	80.5	80.5	80	80	80	79.5	79	79	79
	Result No.		7	m	4	ς.	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21		23	24	25	26	27	28	29

A;Cross-references: UNIPROT:Q8X965; GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GA A;Experimental source: strain 0157:H7, substrain RIMD 0509952 C;Genetics:

3;

Gaps

9 45

46.0%; Score 98; DB 2; Length 394; 65.3%; Pred. No. 0.03; iive 2; Mismatches 9; Indels

Query Match
Best Local Similarity 65.33
Matches 32; Conservative

C;Genetics: A;Gene: ECs0774

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probable rotamase	hypothetical prote	histone H1 - Chlam	histone H1 - tomat	polyhydroxyalkanoa	tolA protein [impo	histone H1.10 - ch	histone H1-5 [vali	invariant surface	probable transfera	histone H1A - Afri	histone H1-II - Vo	TolA colicin impor	ribosomal protein	hypothetical prote	histone H1 - mouse
A81794	829309	\$59589	S45662	G83013	AG0592	A28456	S51660	B38145	B70868	151227	JN0748	AC0138	JC5954	T06636	A28470
7	0	7	7	7	~	7	٦	~	~	~	7	~	7	0	7
347	217	231	287	309	376	220	226	523	580	229	241	388	220	924	212
37.1	36.6	36.6	36.6	36.6	36.4	36.2	36.2	36.2	36.2	35.7	35.7	35.7	35.4	35.4	35.2
79	78	78	78	78	77.5	77	77	77	77	26	16	16	75.5	75.5	75
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Cispeciaes: Lytechinus pictus (painted urchin)
Cispeciaes: Lytechinus pictus
Cispeciaes: Lat. A2550
Nucleic Acids Res. 14, 8121-8133, 1986
A.Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus and A;Reference number: A25550
A;Recession: A25550
A;Accession: A25550
A;MuD:87040778; PMID:302245
A;Accession: A25550
A;Molecule type: DNA
A;Residues: 1-210 <KNO>
A;Cross-references: UNIPROT:P06144; GB:X04488; NID:99616; PIDN:CAA28177.1; PID:99617
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane spanning protein TolA [imported] - Escherichia coli (atrain O157:H7, substrain F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CjAccession: F90725
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G., gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DhA Res. 8, 11-22, 2000
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom A; Reference number: A99629; MUD:21156231; PMID:11258796
A; Status: preliminary
A; Status: preliminary
A; Residues: 1-394 < HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Escherichia coli
Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKAKAEK-AKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.6%; Score 103.5; DB 2;
65.1%; Pred. No. 0.0057;
cive 3; Mismatches 11;
histone H1 - sea urchin (Lytechinus pictus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 65.1 tes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Si
Matches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
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Objective Institution procession amongytogenes (Strain Eduler)

C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AEI317
A;Authors: Kreft, U.
Science 294, 849-852, 2001
A;Authors: Kreft, U.
Science 294, 849-852, 2001
A;Authors: Kreft, U.
Science 294, 849-852, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Attle: Comparative genomics of Listeria species.
A;Reference number: ABI077; WUID:21537279; PMID:11679669
A;Accession: AEI317
A;Accession: BNA
A;A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Listeria innocua
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
Jones, L.M.; Rarst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; Mat
ok, C.; Schlueter, T.; Simces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q92A67; GB:AL592022; PIDN:CAC97285.1; PID:g16414556; GSPDB:G1
A;Experimental source: strain Clipl1262
C;Genetics:
A;Gene: lin2055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein homolog lin2055 [imported] - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                   hypothetical protein lmo1941 (imported) - Listeria monocytogenes (strain EGD-e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---AKYEKAAAEKAAA 38
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دي
                                                              247 KKAAEKAAABEKAAADKKAAAEKAAADKKAAA-AKAAAEKAAAAABA 294
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          Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Best Local Similarity 45.5%; Pred. No. 0.11;
Matches 30; Conservative 3; Mismatches
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Best Local Similarity
Matches 27; Conserv
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A; Status: preliminary
A; Molecule type: DNA
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membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli (Species: Escherichia C;Accession: GB5576
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Accession: GB5576
A;Accession: GB5576
A;Accession: GB5576
A;Accession: GB5576
A;Accession: GB5576
A;Accession: GB576
A;Accession: GB57
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A; Residues: 1-421 < LEV.
A; Residues: 1-421 < LEV.
A; Residues: 1-421 < LEV.
A; Cross-references: UNIPROT: P19934; GB: M28232; NID: g148018; PIDN: AAA24683.1; PID: g148019
A; Experimental source: strain JM105
A; Rose: the authors translated the initiation codon GTG for residue 1 as Val
A; Note: the authors translated the initiation codon GTG for residue 1 as Val
R; Blattner, P.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A; Rose, D.J.; Mau, B.; Slao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID: 97426617; PMID: 9278503
A; Accession: B64810
A; Residues: nucleic acid sequence not shown; translation not shown
A; Residues: 1-421 < BLAT>
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tolA protein - Escherichia coli (strain K-12)

(c)Species: Bscheritchia coli

(c)Species: Bscheritchia coli

(c)Accession: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

(c)Accession: J00057, B64810

(c)Accession: J00057, B64810

(c)Accession: J00057, MUD:90078104, PMID:2687247
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C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t
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9
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Pred. No. 0.03;
2; Mismatches 9; Indels
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46.0%; Score 98; DB 2; Length 421;
Best Local Similarity 65.3%; Pred. No. 0.032;
Matches 32; Conservative 2; Mismatches 9; Indels
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Best Local Similarity 65.3%;
Matches 32; Conservative
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A,Map position: 17 min
A,Start codon: GTG
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요

2

Gaps

7

Molecule type: DNA A; Accession: S34154

Matches

8 셤 RESULT 9

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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Status: preliminary nucleic acid sequence not shown; translation not shown A;Status: 1.214 *COL>
A;Residuse: 1.214 *COL>
A;Cross-references: UNIPROT: P95109; GB:Z83018; GB:AL123456; NID:g3261671; PIDN:CAB05427.)
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: B87553
E;Nierman, W.C.; Feldblyum, T.V.; Pauleen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.!
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolone
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Fitle: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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C;Species: Treponema phagedenis
C;Species: Treponema phagedenis
C;Date: 30-Jan-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C;Date: 30-Jan-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C;Accesion: B43592
R;Yelton, D.B.; Limberger, R.J.; Curci, K.; Malinosky-Rummell, F.; Slivienski, L.; Schoul Infect. Immun. S9, 3685-3691, 1991
A;Fitle: Treponema phagedenis encodes and expresses homologs of the Treponema pallidum Th A;Reference number: A43592; MUID:91372983; PMID:1894368
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A;Cross-references: UNIPROT:P29720; GB:M58563; NID:g155066; PIDN:AAA27480.1; PID:g155067
A;Note: the authors translated the codon TTC for residue 316 as Tyr, and CGA for residue
C;Keywords: membrane protein
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: G70673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 89.5; DB 2; Length 214; Pred. No. 0.11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.6%;
Matches 25; Conservative
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: B87553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Genetics:
A,Gene: CC2451
                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: hupB
                                                                                                                                                                                                                                                                                                                                                                               Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        histone H1-beta, embryonic - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004
C;Accession: A28100
R;Lai, Z.C.; Childs, G.
Mylila: Call. Biol. 8, 1842-1844, 1988
A;Title: Characterization of the structure and transcriptional patterns of the gene A;Reference number: A28100, MVID:88246461; PMID:2837660
A;Molecule type: DNA
A;Residues: 1-211 < Lall > La
                                                                                       sperm tail-specific protein mst101(2) - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Species: Drosophila hydei
C;Species: Drosophila hydei
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 55.364; S34154
R;Neesen, J.; Padmanabhan, S.; Buenemann, H.
R;Neesen, J.; Padmanabhan, S.; Buenemann, H.
A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif: 1pha-helical rods within the extremely elongated spermatozoa of Drosophila hydei.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable hupB - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul.-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: G70673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
C;Genetics: mst101(2)
A;Gene: mst101(2)
A;Cross-references: FlyBase:FBgn0011816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
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C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 89.5; DB 2;
Pred. No. 0.11;
3; Mismatches 10;
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1390 «NEE»
A;Cross-references: UNIPROT:Q08696; EMBL:X73481
R;Neesen, J.; Heinlein, U.A.O.; Buenemann, H.
submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S51364
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
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Best Local Similarity 61.9%;
Matches 26; Conservative
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Search completed: December 14, 2004, 05:52:12
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Best Local Similarity 51.1%;
Matches 24; Conservative
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Best Local Similarity 61.4%;
Matches 27; Conservative
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A.Gene: bpH1
C;Superfamily: histone H1
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E83525
TolA protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Nam, X.O; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, t.; Lory, S.; Olson, M.V.
                                                                                                                                                                          A;Cross-references: UNIPROT:Q11142; GB:Z77162; GB:AL123456; NID:g3261606; PIDN:CAB00936.
A;Experimental source: strain H37Rv
C;Genetics:
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C;Species: Drosophila hydei
C;Species: Drosophila hydei
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34153
R;Neesen, J.; Heinlein, U.A.O.; Buenemann, H.
submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A;Molecule type: mRNA
A;Residues: 1-344 <NEE>
A;Cross-references: UNIPROT:Q08695; EMBL:X73480; NID:g313199; PID:g313200
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                                                                                                                                                       hypothetical protein Rv0475 - Mycobacterium tuberculosis (strain H37RV)
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40.4%; Score 86; DB 2; Length 344;
Best Local Similarity 57.8%; Pred. No. 0.35;
Matches 26; Conservative 3; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 40.4%; Score 86; DB 2; Length 199; Best Local Similarity 65.6%; Pred. No. 0.23; Matches 21; Conservative 4; Mismatches 7; Indels
                         1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYE 44
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A;Cross-references: FlyBase:FBgn0011816
C;Superfamily: neurofilament triplet H protein
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A;Accession: S34153
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A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <STO>
A;Cross-references: UNIPROT:P50600; GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG0436(A;Experimental source: strain PA01
C;Genetics:
A;Genetics:
A;Genetics:
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R;Scarlato, V.; Arico, B.; Goyard, S.; Ricci, S.; Manetti, R.; Prugnola, A.; Manetti, R.; Mol. Microbiol. 15, 871-881, 1995
A;Title: A novel chromatin-forming histone H1 homologue is encoded by a dispensable and c A;Reference number: S61926; MUID:95319329; PMID:7596289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S61926
A;Nolecule type: DA
A;Residues: 1-182 <SCAL>
A;Residues: 1-182 <SCAL>
A;Cross-references: UNIPROT:Q45370; EMBL:L37438; NID:g777717; PIDN:AAB59120.1; PID:g77771
A;Accession: S69327
A;Molecule type: protein
A;Residues: 'X',3-39 <SCA2>
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C;Species: Bordetella pertussis
C;Date: 23-Jul-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
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Pred. No. 0.35;
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Pred. No. 0.26;
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Nature 406, 959-964, 2000
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HI_LYTF1
ID__HI_LYTPI
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                                                                             December 14, 2004, 05:47:53 ; Search time 50.5063 Seconds (without alignments) 512.646 Million cell updates/sec
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version 5.1.6
- 2004 Compugen Ltd.
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Q7NAG18

Q8X965

TOLA ECOLI

Q6M1V1

Q6M1V1

Q6M1V1

Q6M1V1

Q911K6

Q815M1

Q87W3X2

Q97W3X2

Q97W3X2

Q07W3X2

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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Match Length DB
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 w w w w w					Q88NI6 Q7WFA2 Q73D27 AAS39818		Q88ni6 pseudomonas Q7wfa2 bordetella Q73d27 bacillus ce Aas39818 bacillus	co (b) }
2 W W W 4 4	88 86.5 86.5 86.5 86.5	J-10044	1551 200 384 105	300F00	0945J6 07SBU1 08XVN7 TMPB TREPH 06N503	71	Uyasje caulobacter Q7sbul neurospora Q8xvn7 ralstonia s P29720 treponema p Q6n503 rhodopseudo Q4658621 rhodopseudo	H _ 10 CA O Z
 चंच चंच					Q8P140 RS16 COREF HBHA MYCTU	6. 7	QBpi40 xanthomonas QBfp30 corynebacte Q11142 mycobacteri O93946 candida alb	100-10
					ALIGNMENTS	SINE		
SU.	T 1 5 Q7WFN5	PRELIMINARY	NARY;		PRT;	379 AA.		
71000 1000	Q7WFN5; 01-OCT-2003 (7 01-OCT-2003 (7 01-MAR-2004 (7	rembi rembi rembi	rel. 2		Created) Last seque Last annot	Created) Last sequence update) Last annotation update)		
	Proline rich inner membrann OrderedLocusNames=BB4236; Bordetalla bronchiseptica Bacteria; Proteobacteria;	mes=E	membrane 3B4236; septica (. steria; B	(Al	procein. lcaligenes taproteobs	re procein. (Alcaligenes bronchisepticus). Betaproteobacteria; Burkholderiales	;). leriales;	
 3 8 8 8 8 8	Alcaligenaceae; NCBI_TaxID=518; [1]	il8;	decerro					
 8 2 2 X	SEQUENCE FROSTRAIN=RBS0	M N.A. / ATCC 27954; P	BAA-58	8; 1291	0271; 000	[=10.1038/ng1227,	P SEQUENCE FROM N.A. C STRAIN=RBSO / ATCC BAA-588; X MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;	
RA RA	Parkhill J., Harris D.E., Cerdeno-Tari	Sebaih Holden raga A	ia M M.T.G M., Ter	Pre nole	ston A., hurcher (L., Jame	Murphy L.D., The C.M., Bentley S.I es K.D., Harris I	omson N.R., J., Mungall K.L., J., Quail M.A.,	
RAR	Achtman M., Chillingwort	Atkin R	ollins	er s	Cronin P	n D., Bason N., (A., Davis P., Doc	Cherevach I., ggett J.,	
 8 8 8 8 1 1 1	eltwell T., Leather S., Rabbinowits	Moule S	A., Had ., Norl utter	berc	N., наце zak H., С Sanders N	ser H., Holroya : J'Neil S., Ormond M., Saunders D.,	i., Jageis K., 1 D., Price C., Seeger K	
. % B	Sharp S., Si	mmonds itehead	M., Ske	elto	ո J., Տգր 11 B.G.,	nares R., Squares Maskell D.J.;	S., Stevens K.,	
RT	"Comparative Sordetella p	analys	is of ussis	the	genome se Bordetell	equences of Borde la bronchiseptica	etella pertussis, ";	
388	MAL: GEMEL: EMBL; BX6404 30; GO:00160	149; CAE	34600.	H .	ΕΆ.			
 88	30; GO:00302	288; C:p	eripla rotein	emic	space (Ensporter	sensu Gram-negat: activity; IEA.	ve Bact; IEA	i
 ¥	GO; GO: GOLDIS InterPro; II InterPro; II	ISU31; F:procein IPR010528; TolA. IPR006260; TonB	rotein ; ; TolA. ; TonB_(. T.	nsport; 1	LEA.		
		5519; TolA; TIGR01352;		_Cte	Cterm; 1.			
 S CS	SEQUENCE pro	379 AA;	40776 MW;	MW;	C657B5	C657B5AAE97EBDD3 CRC64;		
 Que: Best Matc	Query Match Best Local Simi Matches 28;	h Similarity 65. 28; Conservative	50.9%; 65.1%; ative	ru.	Score 108.5; Pred. No. 0.0 ; Mismatches	Score 108.5; DB 2; Length Pred. No. 0.0073; ; Mismatches 7; Indels	jth 379; els 3; Gaps	1,
 ۶ ج	5 AK	AKKAKAEKAKKAYKAAEAKKAAKYE- : :	KAYKAAI	EAKK	AAKYEF Kakeeaake	AKKAKAEKAKKAYKAAEAKKAAKYE KAAAEKAAAKEAAYE	44 243	
	1						2	
 KESULY Z H1_LYTPI	rp.				!			

210 AA.

PRT;

STANDARD;

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Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A., Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Shabrowitsch E., Rutter S., Sanders M., Sauders D., Seeger K., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Unwin L., Miltehead S., Barrell B.G., Maskell D.J.; "Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica.";
                                                                                                                                                                                                                                                                                                                 373 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  Complete proteome SEQUENCE 373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=1;
                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain
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Matches
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                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                            TISSUE=Embryo;
MEDLINE=87040778; PubMed=3022245;
Knowles J.A., Childs G.J.;
"Comparison of the late H1 histone genes of the sea urchins Lytechinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=12822 / ATCC BAA-587;
MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
Parkhill J., Sebaihia M., Pereston A., Murphy L.D., Thomson N.R.,
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                       Lytechinus pictus (Painted sea urchin).
Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DNA-binding; Multigene family; Nuclear protein. 21746 MW; 08C38F64894007E2 CRC64;
                                                                                                                                                                                                                                     pictus and Strongelocentrotus purpuratus.";
Nucleic Acids Res. 14:8121-8133(1986).
-!- FUNCTION: Histones H1 are necessary for the condensation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 AKKAAKKPAAKKPAKKAAKKPAAKKAAKPAKKAAKKAA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKAKAEK-AKKAYKAAEAKKAAKYEKAAAEKAAAKEAA
                                                                                                                                                                                                                                                                                 nucleosome chains into higher order structures.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the histone H1/H5 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                (Rel. 06, Created)
(Rel. 06, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 103.5; DB Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR005818; Histone H1/H5.
InterPro; IPR005819; Histone H5.
InterPro; IPR003216; Linkerhist N.
InterPro; IPR009058; Wing hlx DNA bnd.
Pfam; PF00538; Linker histone; I.
PRINTS; PR00624; HISTONEH5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proline-rich inner membrane protein.
OrderedLocusNames=BPP3791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD000373; Linkerhist_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X04488; CAA28177.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 65.1
les 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00526; H15; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A25550; A25550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 AA;
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                 NCBI_TaxID=7653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=519;
                                                             Late histone H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P02259;
                              01-JAN-1988
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chromosomal
                                                                                                                     Lytechinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ргодош;
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Q7W477
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Nat. Genet. 35:32-40(2003).

BML; BX640444; CAR39074.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.

GO; GO:0015031; P:protein transporter activity; IEA.

InterPro; IPR010528; TolA.

InterPro; IPR006560; TonB_C.
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYA--KKAKAEKAKK--AYKAAEAKKAAKYE---KAAAEKAAAKEAAYE 44
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H
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Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
                                                                                                                                                                                                                                                                                                                                             DB 2; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodopirellula baltica.
Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.2%; Score 98.5; DB 2; Length 461; 57.8%; Pred. No. 0.084; cive 5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome; Hypothetical protein; Repeat; TPR repeat.
SEQUENCE 461 AA; 50441 MW; A7C5752864CBE14C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KKY-AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA
                                                                                                                                                                                                                                                                                         40092 MW; A364894DAE46E328 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                       Amatch 48.6%; Score 103.5; DB Local Similarity 62.7%; Pred. No. 0.022; Nes 32; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.084
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                    TIGRFAMs; TIGR01352; tonB_Cterm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BX294143; CAD74436.1; -.
InterPro; IPR001440; TPR.
Pfam; PF00515; TPR; 7.
SMART; SM0028; TPR; 7.
PROSITE; PS50005; TPR; 4.
PROSITE; PS50293; TPR_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
Hypothetical protein.
OrderedLocusNames=RB5786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 57.8
Matches 26; Conservative
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                                                                                                                                                                                                                 Pfam; PF06519; TolA;
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32; Conservative
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Tola protein.
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                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21074935, PubMede=11206531,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Poste D.J., Mayhew G.F., Evans P.S., Gregor J., Kirbatrick H.A.,
Postei G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                          Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Membrane spanning protein, required for outer membrane integrity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF06519; TolA; 1.
SEQUENCE 394 AA; 40517 MW; 5B58D8E8230BDE28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40517 MW; 5B58D8E8230BDE28 CRC64;
                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) membrane spanning protein TolA. OrderedLocusNames=ECS0774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 98; DB 2;
Pred. No. 0.081;
                                                         394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-0157:H7 / RIMD 0509952 / EHEC;
MEDLINE-21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=tolA; OrderedLocusNames=20907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Escherichia
NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP002553; BAB34197.1; -. InterPro; IPR010528; TolA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.0%;
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PIR; F90725; F90725.
PIR; G85576; G85576.
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nes 32, Conservative
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                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
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                                                                                       Q7AGI8;
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                                                            Q7AG18
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Length 394;

46.0%;

Query Match

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X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421.
MEDLINE=99332679; PubMed=10404600;
Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.;
Filamentous phage infection: crystal structure of g3p in complex with its coreceptor, the C-terminal domain of TolA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levengood S.K., Webster R.E., "Nucleotide sequences of the tolA and tolB genes and localization of their products, components of a multistep translocation system in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAID=KIZ / MG1652.
STRAID=KIZ / MG1652.
STRAID=KIZ / MG1652.
STRAID=KIZ / MG1652.
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Maynew B., Shao Y., Bavis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97133271; PubMed=8978668;
Derouiche R., Gavioli M., Benedetti H., Prilipov A., Lazdunski C.,
                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levengood S.K., Beyer W.F. Jr., Webster R.E.; membrane protein involved in colicin uptake contains an extended helical region."; M. 88:5939-5943 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                    9
                                                                               220 KKAAEKAAAEKAAADKKAAAEKAAADKKAAA-AKAAAEKAAAAKAAAEA 267
                                                      45
                                                                                                                                                                                                                                                                                                                 Name=tolA; Synonyms=cim, excC, lky; OrderedLocusNames=b0739;
                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "TolA central domain interacts with Escherichia coli
EMBO J. 15:6408-6415(1996).
65.3%; Pred. No. 0.081; ive 2; Mismatches
                                                                                                                                                                                           TOLA_ECOLI STANDARD; PRT; 421 AA. P19934; 01-FEB-1991 (Rel. 17, Created) 01-FEB-1991 (Rel. 17, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriol. 171:6600-6609(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90078104; PubMed=2687247;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.",
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Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C., Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F., Scokett R.E., Schuster S.C., "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S.-R., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete genome sequence of uropsthogonic Bacherichia coli.", Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bdellovibrio bacteriovorus.
Bacteria, Proteobacteria, Deltaproteobacteria, Bdellovibrionales,
Bdellovibrionaceae, Bdellovibrio.
                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 KKAABEKAAABEKAAABKKAAABKAAABDKKAAA-AKAAABKAAAAKAAABA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.8%; Score 95.5; DB 2; Length 198; 58.7%; Pred. No. 0.076; ive 4; Mismatches 14; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.0%; Score 98; DB 2; Length 421; 65.3%; Pred. No. 0.086; ive 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome; Hypothetical protein.
SEQUENCE 198 AA; 20875 MW; 9942AF2CD8D653D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 AA; 43184 MW; DB296626F056D385 CRC64;
                                                                                                                                          Last sequence update)
Last annotation update)
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STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
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                                         421 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
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                                                                                                         Created)
                                         PRT;
                                                                                                                                                                                                                                                    Name=tolA; OrderedLocusNames=c0818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic perspective.";
Science 303:689-692(2004).
BmBL; BX842654; CAE80819.1; -
INTERFPC; IRR005819; Histone H5.
PRINTS; PRO0624; HISTONEHS.
                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae; Escherichia
NCBI TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 165-JUL-2004 (TrEMBLrel. 27, 14) Thypothetical protein.
OrderedLocusNames=Bd3054;
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Conservative
                                                                       Q8FJT1;
01-MAR-2003 (TEMBLEE]. 23,
01-MAR-2003 (TEMBLEE]. 23,
01-MAR-2004 (TEMBLEE]. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR010528; TolA. Pfam; PF06519; TolA; 1.
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Matches 27; Conservative
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                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                             Escherichia coli 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P19934; 1TOL.
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Matches 32, Conserv
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                                                                                                                                                                                                                      Tola protein.
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Q6MIU4;
                                 QBFJT1
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                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
13 tandem repeats of [EDA]-K(1,2)-A(2,4).
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                              FUNCTION: Involved in the tonB-independent uptake of group A colicins (colicins A, B1, E2, B3, and K). Necessary for the colicins to reach their respective targets after initial binding to the bacteria. Also involved in the translocation of
                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                     Dacteriophage DNA.
SUBUNIT: Interacts, via domain II, with porins ompC, phoE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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Pred. No. 0.086;
2; Mismatches 9; Indels
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EMBL; D90713; BAA35405.1; -.
PIR; JV0057; JV0057.
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Best Local Similarity 65.3%;
Matches 32; Conservative
Structure 7:711-722(1999)
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"Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
EMBL; AE015086; AAN42202.1; -..
INTERPROS. 170L.
INTERPROS. 1PR010528; TOLA.
Pfam; PP06519; TOLA.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Sheng J., Yang G., Wu H., Qu D., Dong J.,
Yang T., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE_21537279; PubMed=11679669;
MEDLINE=21537279; PubMed=11679669;
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann B., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsinh H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gonmez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ny B., Nedjari H.,
Rodueno E., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoss N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                       083SA1,
01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
membrane spanning protein, required for outer membrane integrity.
Name=tolA; OrderedLocusNames=SF0558;
Shigella flexneri.
                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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OrderedLocusNames=lmo1941;
                                                                                                                                                      PRELIMINARY;
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Best Local Similarity
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                                                                                                            RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22590274; PubMed=12704152; Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Pournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T."; Infect. Immun. 71:275-2786 (2003).

EMBL; ABO16979; AAP16075.1; -.. InterPro; IPR010528; TolA.

Elem; PPO5519; TolA.; I.
                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
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Enterobacteriaceae; Shigella.
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44.6%; Score 95; DB 2; Length 413; 63.3%; Pred. No. 0.17; tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 AAKPAKKATAKKAAKPAKKAAPKKAAKPAKKAAPKKAAVKKAAKPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 198 Aa; 20875 MW; 9942AF2CD8D653D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42355 MW; 93E10F2C5DE60DE8 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
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                                                                                                                                198 AA
                                                                                                                                                                          Created)
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Name=tolA; OrderedLocusNames=S0571;
Shigella flexneri.
                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic perspective.";
Science 303:689-692(2004).
EMBL; BX842654; CAE80819.1; -.
                                                                                                                                                                   02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                             Bdellovibrio bacteriovorus.
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les 27; Conservative
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Matches 31, Conservative
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                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                     Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=14752164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=623;
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=959;
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MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Golteman B., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.C.;
Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
Nature 423:87-91(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             44.4%; Score 94.5; DB 2; Length 239; 56.2%; Pred. No. 0.11; ive 7; Mismatches 9; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                             43.9%; Score 93.5; DB 2; Length 248; 50.9%; Pred. No. 0.15; ive 4; Mismatches 9; Indels 15
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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SEQUENCE 248 AA; 27107 MW; F056965438077925 CRC64;
                                                                                                                                                                                                                                                         72E59D576E0D7832 CRC64;
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Last annotation update)
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Last annotation update)
genomics of Listeria species.";
                  Science 294:849-852(2001).
EMBL; AL511981; CAD00019.1; -.
PIR; AB1317; AE1317.
GO; GO:0016998; P:cell wall catabolism; IEA.
InterPro; IPR002482; LysM.
Pfam; PF01476; LysM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 AA
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STRAIN-USDAI10;
MEDLINE-22484998; PubMed=12597275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Last CAA-E operon negative regulator. ORFNames=BC0954;
                                                                                                                                                                                                                                                         239 AA; 25836 MW;
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(TrEMBLrel. 24, L
(TrEMBLrel. 24, L
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                                                                                                                                                                                                                                                                                                                                   Local Similarity 56.2
les 27; Conservative
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les 29; Conservative
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                                                                                                                                                                                                                                 Complete proteome.
SEQUENCE 239 AA;
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  "Comparative
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Matches 29
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Best Local S
Matches 27
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; Search time 49.7468 Seconds (without alignments)
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Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
GenCore (c) 1993
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries genesemp2001s:* genesemp2002s:* genesemp2003as:* genesemp2003bs:* genesemp2004s:* A_Geneseq_23Sep04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* Database :

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Description	Toront Theorem	Aay82572 Copolymer	Aay82577 Copolymer	-	-	-	-	•	Aay82571 Copolymer		Aar28871 High affi	Abu28559 Protein e	Abu31397 Protein e	Abo67048 Klebsiell	Abb49123 Listeria	Abu32619 Protein e	Aar06445 Recombina	Aay14928 Amino aci	Abp70903 Mycobacte	-	Aay57353 M. tuberc	Abu34623 Protein e	Abu36893 Protein e	Abu40185 Protein e	Abg28693 Novel hum	_
SUMMARIES		AAY82572	AAY82577	AAY82573	AAY82575	AAY82576	AAY82574	ABU27824	AAY82571	AAR06446	AAR28871	ABU28559	ABU31397	AB067048	ABB49123	ABU32619	AAR06445	AAY14928	ABP70903	AAY34055	AAY57353	ABU34623	ABU36893	ABU40185	ABG28693	NAWA 402A
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Scool	1000	213	138	134.5	131	126.5	120.5	108.5	108	99.5	98	98	95	95	94.5	94.5	94	91	91		89.5	89.5	89.5	88.5	87	ď
Result	2	т	7	e	4	ស	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

-	Aaw43082 Mycobacte	Aaw44936 Mycobacte	Abu38313 Protein e	Abj18771 Pseudomon	Abo80835 Pseudomon	Aab20575 Mycobacte	Aag70868 C albican	Adp99051 C. albica	Abu39221 Protein e	Aag91997 C glutami	_	Adh88105 Enterococ	Abg71044 Tumour ne	Abu47123 Protein e	Abu33811 Protein e	Abu22879 Protein e	Abu26064 Protein e	Abo23523 Pseudomon	Abo84211 Pseudomon
ADF45561	AAW43082	AAW44936	ABU38313	ABJ18771	ABO80835	AAB20575	AAG70868	ADP99051	ABU39221	AAG91997	ABM67869	ADH88105	ABG71044	ABU47123	ABU33811	ABU22879	ABU26064	AB023523	AB084211
7	~	7	9	9	7	m 	4	80	9	4	9	7	5	9	9	9	9	7	7
ε.	198	198	347	347	407	205	427	427	385	165	357	497	8	407	212	875	157	309	316
40.4	40.4	40.4	40.4	40.4	40.4	40.1	39.9	39.9	39.0	38.5	38.3	38.3	38.0	37.3	37.1	36.9	36.6	36.6	36.6
86	86	98	98	86	98	85.5	82	85	83	82	81.5	81.5	81	79.5	79	78.5	78	78	78
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

glatitamer accate; autoimmune disease; antiarthrittic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatory; antitanaemic; immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2. Copolymer; molecular weight marker; TV-marker; immune disease; AAY82572 standard; peptide; 45 AA. (first entry) 28-JUL-2000

WO200018794-A1. Unidentified. 06-APR-2000,

99WO-US022402. 98US-0101693P. 25-SEP-1998; 24-SEP-1999;

(YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; Gad A,

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention of escribes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

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of the invention are used as molecular weight markers for glatiramer actate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thrombocytopaenia purpura, colitis, coneat sensitivity disease, dispetse mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic luque erythematoous. Mediated. mediated diseases which can be treated include host versus-graft disease, and delayed-type hypersensitivity. The colypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which communicated markers
            $$$$$$$$$$$$$$$$$$$$$$
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Sequence 45 AA;

Gaps . 0 Length 45; 1 AKKYAKKAKAKAEKAKKAYKAABAKKAAKYEKADAEKAAAKEAAYEA 45 1 AKKYAKKAKAKAEKAYKAYBABAKKAAKYEKAAAEKAAAKEAAYEA 45 0; Indels 100.0%; Score 213; DB 3; 100.0%; Pred. No. 3.2e-16; 0; Mismatches 셤

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RESULT 2 AAY8257

AAY82577 standard; peptide; 109 AA.

AAY82577;

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarhitic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidiabetic; thyromimetic; hemostatic; antipsoriatic; dermatological; antidiabetic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified.

WO200018794-A1

06-APR-2000.

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Gad A, Lis D;

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

Claim 10; Page 14; 72pp; English

AAY82571 to AAY82577 represent specifically claimed copolymer molecular

weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an an among animo acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer caetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating diseases such diseases include arthritic conditions, demyelinating carthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune arthritis, autoimmune thrombocytopania purpura, colitis, contact cophoritis, autoimmune thrombocytopania purpura, colitis, contact sansitivity disease, diabetes mellitus, Graves disease, diabetes mellitus, Graves disease, diabetes mellitus, Graves disease, chronic immune thrombocytopania purpura, colitis, contact sansitivity disease, diabetes mellitus, Graves disease, dialetes mellitus, Graves disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined melecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers 3 Gaps 4 65 akkyakaakae--kkeyaaaeakkaeaakaykaeaakaaakeaayea 109 Length 109; Score 138; DB 3; Lengtn Lv. Pred, No. 1.1e-07; 64.8%; Sco... 76.6%; Pred. No. 1... 0; Mismatches Ą AAY82573 standard; peptide; 56 Query Match Best Local Similarity 76.67 Matches 36; Conservative Sequence 109 AA; AAY82573; AAY82573 셤

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyrominetic; hamemostatic; antipsoriatic; dermatological; antidamenic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple solerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Hashimoto's THE STATE OF THE S

Unidentified.

WO200018794-A1

06-APR-2000.

99WO-US022402. 24-SEP-1999;

98US-0101693P 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; Gad A, WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

WPI; 2000-317499/27.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determaining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glattramer cot acetate related terrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell mediated or antibody-mediated diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroidmins, e.g. multiple sclerosis, contact cophoritis, autoimmune thrombocytopeania purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, dispetes mellitus, Graves disease, dispetes mellitus, Graves disease, dispetes mellitus, graves disease, mediated diseases which can be treated include host-versus-graft disease, chronic disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer accetate molecules, which

Sequence 56 AA;

1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKY - KAEAAKAAAKEAAYEA 56 Gарв 13; ch 63.1%; Score 134.5; DB 3; Length 56; 1 Similarity 68.4%; Pred. No. 1.4e-07; 39; Conservative 0; Mismatches 5; Indels 1: .5; _____. .1.4e-07; Best Local Similarity Matches 39; Conserv Query Match ð g

4

AAY82575 standard; peptide; 77 AA AAY82575; AAY82575
AAY8257
AAY825

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiartici; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; heamostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; theumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified

WO200018794-A1.

06-APR-2000

99WO-US022402. 24-SEP-1999; (YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Gad A, Lis D;

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AMYR812, TO ABYR812// TEPPERSENT SPECIALIZALLY CLARINGEN CONFORTAGE.

WANTER TO SPECIAL SECONDARY SECONDARY AND AND ASSET AND AND ABYR812/ TRANSPRICE PROPERTY.

To de acopolymer (CPP), which has an identified molecular weight and an among acid composition corresponding to the copolymer. The polypeptides are neated as molecular weight markers for glatizamer of the invention are used as molecular weight markers for glatizamer.

To the invention are used as molecular weight markers for glatizamer of the invention are used as molecular weight markers for glatizamer.

TO treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, a service arthritis, autoimmune hamonitis, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune hamoniditis, autoimmune thyroiditis, autoimmune thyroididis, e.g. multiple sclerosis, forbn's clisease, chronic immune thyroididis, graves disease, Guillain-Barre's clisease, chronic immune thrombocytopeania purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxocedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-contains, phost disease, and delayed-type hypersensitivity. The properties which are analogous to glatizamer acetate molecules, which makes them ideal for use as molecular weight markers
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                                                                                                                                                                                                AAV82571 to AAV82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present
                                             Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKK----AKAEKA----KKAYKAAEAKKAAKYE-----AKAEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.5%; Score 131; DB 3; Length 77;
50.6%; Pred. No. 4.6e-07;
ive 0; Mismatches 6; Indels 32; Gaps
                                                                                                                                         Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 50.6
hes 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 77 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
8
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30 -KAAAEKAAAKEAAYEA 45 || || || || || || || 61 1 YKAEAAKAAAKEAAYEA 77

RESULT 5 **AA**Y82576

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AAY82576 standard; peptide; 86 AA. 28-JUL-2000 (first entry) AAY82576;

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; nemenostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

WO200018794-A1

06-APR-2000.

99WO-US022402. 24-SEP-1999;

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glattramer act actate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases catter related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases of diseases such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, cronn's disease, chronic immune thyroidments haemolytic ansemia, autoimmune coophoritis, autoimmune thyroidments, disease, disease, disease, disease, dispetes mellitus, Graves disease, disease, shinch can be treated include host-versus-graft disease, sporiasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, colypeptides of the invention have defined molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                              Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 126.5; DB 3; Length 86;
Pred. No. 1.6e-06;
0; Mismatches 6; Indels 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKK-----AKAEKA-----KKAYKAAEAKKAAKYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 УКАЕЛАККАУКАЕЛАКАЛАКЕЛАЎЕЛ 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 -----KAAAEKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ź
                                                                                                                                                                                                                                                             Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY82574 standard; peptide; 66
                                                     (YEDA ) YEDA RES & DEV CO LTD (TEVA-) TEVA PHARM USA INC.
                    25-SEP-1998; 98US-0101693P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 45.3%;
Marches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000 (first entry)
                                                                                                                                                         WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 86 AA;
                                                                                                                  Gad A, Lis D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY82574;
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Gaps

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Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

(YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

WPI; 2000-317499/27.

Lis D;

3ad A,

98US-0101693P. 99WO-US022402,

24-SEP-1999; 25-SEP-1998;

WO200018794-A1

06-APR-2000

Unidentified.

Claim 10; Page 14; 72pp; English

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer cactate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases of treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include either cell-mediated or antibody-mediated diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid diseases and inflammatory conditions, e.g. multiple sclerosis, cronner cophoritis, autoimmune thyroidmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroidmune uveoretnitis, contact carbritis, osteoarthritis, autoimmune byroidmune sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic mysoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, caratre versus-host disease, and delayed-type hypersensitivity. The propperties which are analogous to glatiramer acetate molecules, which are analogous to glatiramer acetate molecules, which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 AKKYAKAKAE--KKEYAAAEAK-----YKAEAAKAAKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by Prokaryotic essential gene #13351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.6%; Score 120.5; DB 3; Best Local Similarity 71.1%; Pred. No. 5.4e-06; Matches 32; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU27824 standard; protein; 428 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU27824;
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WO200277183-A2.

7

Gaps

7;

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(first entry)

28-JUL-2000

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ftp.wipo.int/pub/published_pct_sequences
                                                         Malone C,
Carr GJ,
                  21-MAR-2001; 2001US-00815242.
06-SBT-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342223P.
08-FBB-2002; 2002US-00072851.
                                      06-MAR-2002; 2002US-0362699P.
         21-MAR-2002; 2002WO-US009107
                                                (ELIT-) ELITRA PHARM INC.
                                                         Zamudio C,
Trawick JD,
                                                                       2003-029926/02
                                                                           N-PSDB, ACA31694
                                                                                                                                                                                                                                                                             Sequence 428 AA;
03-OCT-2002
                                                         Wang L,
Wall D,
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50.9%; Score 108.5; DB 6; Length 428; 60.4%; Pred. No. 0.00074; ative 2; Mismatches 8; Indels 11; Local Similarity 60.4 nes 32; Conservative Query Match

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Gaps

AAY82571 standard; peptide; 35 AA. AAY82571; AAY82571 ID AAY XX AC AAY XX

RESULT 8

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AAR06446

RESULT

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Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; antidiabetic; thyromimetic; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                   Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200018794-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lis D;
                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gad A,
the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or polypeptide of its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, (7) identifying a compound that inhibits proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or collection of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. Dientifying proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, CC the target prokaryotic essential genes. Note: The sequence is encoded by one of the target prokaryotic essential essential escource is encoded by one of the circuit of format directly from WIPO at encoded the printed for this collection of the printed specification, but was obtained for the printed for the printed for the printed spec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                            Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                            Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                            Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                         Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 55748; 1766pp; English
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99WO-US022402. 98US-0101693P.

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AMANSALY, TO ARAYSALY, Tepersent Specifically Calmided Copolymer Molecular Weight TV-marker polypeptides (1) for determining the molecular weight for any oppolymer (CP), which has an identified molecular weight and an any oppolymer (CP), which has an identified molecular weight and an any of the invention are used as molecular weight markers for glatizamer of the invention are used as molecular weight markers for glatizamer of the invention are used as molecular weight markers for glatizamer acterated tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases include arthritic conditions, a demyelinating diseases include arthritic conditions, a utoimmune become include arthritis, autoimmune haemolytic anaemia, autoimmune of arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, contact consistivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, permitiated diseases which can be treated include host-versus-graff disease, conjugated disease, and delayed-type hypersensitivity. The collapsetides of the invention have defined molecular weights and physical properties which are analogous to glatizamer acetate molecules, which are assented include markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                               AAY82571 to AAY82577 represent specifically claimed copolymer molecular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.7%; Score 108; DB 3; Length 35; 64.4%; Pred. No. 6.5e-05; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity 64.4%;
29; Conservative
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Best Local Similarity
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glycopeptide; mannose; mannosylated; glycosylated; mannose receptor; macrophages; monocytes; deetroy; cytotoxicity; label; image; alter; macrophages processing of antigen; MFC restriction; inflammation; inflammatory diseases; macrophage secretory products; Crohn's disease; legionnaires disease; mononuclear phagocytes; HIV; AIDS; lysosomal storage diseases; Gaucher's disease; acthma; alveolar macrophages metastasis; systemic macrophages; deliver; antigenic peptides; prevent transplant rejection; organ transplantation; antitumour agents; cancer; toxins.
                                                                                                                                                                                                                                                                                                         /note= "opt may have mannose, fucose, glucose or N-Ac-
glucosamine. May also have non interfering substits."
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glucosamine."
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glucosamine. May also have non interfering substits."
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glucosamine."
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   High affinity macrophage mannose receptor ligand compound #9
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glucosamine."
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glucosamine."
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glucosamine."
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glucosamine,
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                                                                                                                                                                                                                                Synthetic
   To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-19494 US4691009, NREL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-clus cocurs between the Protein A and rCOP-1 sequences. A methionine residue cocurs between the Protein A and rCOP-1 sequences, originating from the cocurs between the Protein A and rCOP-1 sequences, originating from the cocurs between the Protein A and rCOP-1 polypeptide may be cleaved from the fusion protein. TCOP-1-19 contains oligonucleotide duplexes incoding the following segments: YKK, AAE, KAK, EKA, KAA, XEA, AKA KEA, and AAA. The Neternial alanine residue is left behind following CNBr cleaves of the fusion protein. The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain effects on damaged hair or as supplements for diets deficient in certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                      Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 99.5; DB 2;
Pred. No. 0.0017;
4; Mismatches 7;
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AAR06446 standard; protein; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 12; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR28871 standard; peptide; 46 AA
                                                                                                                                                                                                                                                                                                                                                                             89US-00312541
90US-00473845
                                                                                                                                                                                                                                                                                                                                            90EP-00301700
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Best Local Similarity 58.3%;
Matches 28; Conservative
                                                                                               (first entry)
                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                    (REPK ) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-255848/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 106 AA;
                                                                                                                                                                                                                                                                                                                                          16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                             17-FEB-1989;
07-FEB-1990;
                                                                                                                                                                    Recombinant
                                                                          25-MAR-2003
03-JAN-1991
                                                                                                                                                                                                                                                                                                     22-AUG-1990
                                                                                                                                                                                                                                                               EP383620-A
                                                                                                                                                                                                                              Synthetic
                                       AAR06446;
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AAR28871
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N-AC-

fucose, glucose or

or

fucose, glucose

92WO-US003609 91US-00694983

(UNIW) UNIV WASHINGTON

03-MAY-1991; 01-MAY-1992;

(revised)
(first entry)

25-MAR-2003 23-MAR-1993

AAR28871;

CXXXXEEX,

g ð

or N-Ac

fucose, glucose

or N-Ac

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macrophages harbour replicating infectious agents eg. Legionnaires disease; viral infections involving mononuclear phagocytes eg. HIV and lysosomal storage diseases, in which macrophages are principally involved eg. Gaucher's disease; asthma mediated by alveolar macrophages; and in controlling metastasis, mediated by systemic macrophages. The peptides are an also be used to deliver antigenic peptides as conjugates to a macrophage to marshal an immune response; also self peptides to prevent tissue transplant rejection. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                      This compound represents a glycopeptide effective in inhibiting the binding of labelled mannosylated BSA to mannose receptors. Mannose receptors are uniquely found on macrophages and non on monocytes. Glycopeptides such as this provide a mechanism to target macrophages specifically, to image, label, destroy or otherwise alter their antigen processing function. In addition they can be conjugated to solid supports and used to purify mannose receptors from a variety of sources. They are useful in the treatment of inflammatory diseases driven by macrophage secretory products eg. Crohn's disease; infectious diseases in which
                                                                                    New high affinity mannose receptor ligand cpds. - for treating diseases mediated by macrophage activity e.g. asthma, inflammatory diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.0%; Score 98; DB 2; Length 46; 63.4%; Pred. No. 0.001; ive 1; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck R, Ohlsen KL,
Yamamoto R, Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #14086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU28559 standard; protein; 421 AA
                                                                                                                                                          Claim 3; Page 21; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malone C,
Carr GJ,
                                                                                                                       infectious diseases, e.g. HIV.
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-032923P.
08-FEB-2002; 2002US-03022851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002WO-US009107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 63.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ELIT-) ELITRA PHARM INC.
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Trawick JD,
                                                   WPI; 1992-398516/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 46 AA;
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                Stahl PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid nucleic acid, (2) a host cell containing the vector; (3) an isolated condition and propertied or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding cell polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene product or that has an activity against a gene product or that the set of cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) prolifing a compound's activity; (11) a culture comprising strains in which the gene or which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a product is overexpressed or underexpressed, (12) determining the extent compound's activity; (11) a culture compound that inhibits to be strains; or (13) identifying the target of a compound that inhibits the collection of an organism. The antisense nucleic acids are useful for for collectional containing proteins or screening for homologous nucleic acids required for collectional for collection and collection of an organism. The antisense nucleic acids are useful for for collection of the collection of the collection of an organism. The antisense nucleic acids are useful for for collection of the collection of the collection of the collection of the collection of collection of the collection of 
                                               New antisense nucleic acids, useful for identifying proteins or screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                       for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein encoded by Prokaryotic essential gene #16924.
                                                                                                                                                     Claim 25; SEQ ID NO 56483; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU31397 standard; protein; 323 AA
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06-SEP-2001; 2001US-00948993.
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nes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klebsiella pneumoniae
N-PSDB; ACA32429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 421 AA;
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Wang Wall

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The invention describes a new isolated nucleic acid encoding a Klebsiella pheumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a call comprising the recombinant expression evector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preparing a vaccine composition against Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.6%; Score 95; DB 7; Length 469; 52.9%; Pred. No. 0.024; ive 4; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 13565; 932pp; English
                                                                                                                                                                                                                                                                                              (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2001; 2001WO-FR001118.
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                                                                                                                                                                                    27-JAN-2000; 2000US-00489039
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Best Local Similarity 52.9%
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                           Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                   Breton GL, Osborne M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the invention fractace to an isolated muchet acts comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated of polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide of product or that activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or organism acts; (9) manufacturing an antibiotic strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for strains; or (13) identifying the target of a compound that inhibits the confound for proliferation to sellate compound that inhibits are useful for cellular proliferation in cells other than S. aureus, S. typhimurium, K. prequired for proliferation in cells other than S. aureus, S. typhimurium, K. prequent did not form part of the printed specification, but was obtained for the printed specification, but was obtained for the printed specification, but we sade activity and proper sections of the printed specification.
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                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                           Zyskind JW;
Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to an isolated nucleic acid comprising any
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                                                                                                                                                           Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 95; DB 6;
Pred. No. 0.016;
                                                                                                                                                           Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID NO 59321; 1766pp; English
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                                                                                                                                                           Malone C,
Carr GJ,
                      08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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25-OCT-2001; 2001US-0342923P
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Best Local Similarity 52.9°
Matches 27; Conservative
                                                                                                      (ELIT-) ELITRA PHARM INC.
                                                                                                                                                         Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                         2003-029926/02
                                                                                                                                                                                                                                                             N-PSDB; ACA35267
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Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P, Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA, Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
                                                                                                                                                                                                                                       Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                  242 AAEAQKKAEAAAAKKAQQEAEKKAQQEAAKQAAAEKAAAEKAAAKKAAAQKA 292
45
                                                                                                                                                                                                           Listeria monocytogenes protein #1827.
                                                                                                            ABB49123 standard; protein; 239 AA
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Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.

Klebsiella pneumoniae polypeptide seqid 13565.

RESULT 13
ABG67048
ID ABG67048
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DT 29-JU
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KX
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KCCOM
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KCCOM
KW
KRECOM

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The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present invention. Proteins encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and cor by an expense of the present in the sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. concoptogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the vaccines composition for the present did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                         omic sequence for Listeria monocytogenes, useful e.g. for treatment prevention of Listeria and related bacterial infections, and related
     Kaerst U, Entian K,
                                                                                                                                                                                                                          Claim 6; SEQ ID NO 1828; 192pp; French.
Wehland J,
  De Pablos B,
                                                                         WPI; 2002-010914/01.
                                                                                                                         Genomic sequence
                          Voss H;
                                                                                                                                                                              polypeptides.
     Maduenio E,
                             Rose M,
                                                                                                                                                      and
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44.4%; Score 94.5; DB 5; Length 239; 56.2%; Pred. No. 0.014; Live 7; Mismatches 9; Indels Local Similarity 56.2 les 27; Conservative Sequence 239 AA; ~ Query Match Matches 8

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Gaps

5

Protein encoded by Prokaryotic essential gene #18146. ABU32619 standard; protein; 239 AA 19-JUN-2003 (first entry) Listeria monocytogenes ABU32619; RESULT 15

Antisense; prokaryotic essential gene; cell proliferation; drug design.

WO200277183-A2

03-OCT-2002.

21-MAR-2002; 2002WO-US009107

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342223P. 08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P (ELIT-) BLITRA PHARM INC. Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, 'n, Wang | Wall

WPI; 2003-029926/02

N-PSDB; ACA36489

Hauf J;

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 60543; 1766pp; English

The inventor relates to an interact actual completely any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a propertied whose expression is inhibited by the antisense compounds a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense confidence acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular proliferation or the activity of a gene in an operon required for the polypeptide; (5) producing the polypeptide; (6) inhibiting callular compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits callular proliferation; (8) identifying a gene required for callular proliferation of the gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity, (11) a culture comprising strains in which the extent or organism acts; (1) identifying the target of a compound that inhibits the crompound; or the strains is present in a culture or collection of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the critical dentifying proteins or screening for homologous nucleic acids are useful for for callular proliferation of some contains or screening for homologous nucleic acids are quired for callular proliferation of some contains or screening for homologous nucleic acids are qualized. drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences The invention relates to an isolated nucleic acid comprising any

Sequence 239 AA;

Gaps ٠. ک DB 6; Length 239; 44.4%; Score 94.5; DB 6; Length 2 56.2%; Pred. No. 0.014; ive 7; Mismatches 9; Indels Local Similarity 56.2 nes 27; Conservative Query Match Best Loc Matches

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Search completed: December 14, 2004, 06:01:11 Job time : 52.7468 secs

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Sequence 3, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 55748, A
Sequence 59321, A
Sequence 59321, A
Sequence 60543, A
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143.965 Million cell updates/sec
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1 AKKYAKKAKAEKAKKAYKAA......AKYEKAAAEKAAAKEAAYEA 45
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(cgn2_6/ptodata1/1/pubpaa/US07_NEW_PUB.pep:*
(cgn2_6/ptodata1/1/pubpaa/US06_PUBCOMB.pep:*
(cgn2_6/ptodata1/1/pubpaa/US06_PUBCOMB.pep:*
(cgn2_6/ptodata1/1/pubpaa/US07_NEW_PUB.pep:*
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(cgn2_6/ptodata1/1/pubpaa/US09_NEW_PUB.pep:*
(cgn2_6/ptodata1/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-816-989A-7
US-09-816-989A-3
US-09-816-989A-5
US-09-816-989A-4
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US-10-282-122A-55748
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US-10-282-122A-59321
US-10-282-122A-60543
US-10-051-649-201
US-10-205-979-52
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                                                                                                                                                                                                                                                                                                                                                            1585576 seqs, 357178320 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Applications AA:
                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                  Perfect score:
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No.
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	Seguence 6		o							a)															Sequence 1	Sequence 5	Sequence 4	Sequence 6	Sequence 3	Sequence 3	Sequence 3
-10-229-5	US-10-282-122A-62547	۲.	US-10-282-122A-68109	US-10-127-032-120	_	US-10-156-761-9889	US-10-282-122A-67145	US-10-767-701-45061	US-09-738-626-5751	0-425-115	US-10-425-114-37076	0-437-963	.0-282-	10-282-122A-	9	US-10-282-122A-53988	_	_	$\overline{}$	10-156-761-	-01	US-10-229-567-39	US-10-437-963-103091	10-229-	US-10-437-963-169367	10-282-	10-229-	US-10-767-701-60774	-10-229-567-	-567-3	US-10-733-878-381
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ALIGNMENTS

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REBULT 1
US-09-816-989A-2

1 Sequence 2, Application US/09816989A

1 Sequence 2, Application US/09816989A

1 Sequence 2, Application US/09816989A

2 Patent NO. US2020215103A1

2 APPLICANT: Gad, Alexander

3 APPLICANT: Gad, Alexander

4 APPLICANT: Gad, Alexander

5 APPLICANT: Gad, Alexander

5 APPLICANT: Lib Doris

7 TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT WARKI

7 TITLE OF INVENTION: COPOLYMER: US/09/816,989A

CURRENT APPLICATION NUMBER: US/09/816,989A

FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT APPLICATION NUMBER: FOLIO1,693

PRIOR APPLICATION NUMBER: PATON NUMBER: PA
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RESULT

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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE TITLE OF INVENTION: AND FOR THERAPEUTIC USE TITLE OF INVENTION: AND FOR THERAPEUTIC USE TILE REFERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: 0.09/816,989A CURRENT PILING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR APPLICATION NUMBER: 90/101,693 PRIOR PILING DATE: 1999-09-24 NUMBER OF SEQ ID NOS: 7 SOFTWARE: PALCHING VERSION 3.1 SOFTWARE: PALCHIN VERSION 3.1 SOFTWARE: PALCHIN VERSION 3.1 SEQ ID NO 5 LENGTH: 177
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Gad, Doris
TITLE GA, DORIS
TITLE OF INVENTION: COOLUMER: 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: 02/10/93
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR PAPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
REOR FILING DATE: 1999-09-34
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 86
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| AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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45.3%; Pred. No. 1.6e-06;
tive 0; Mismatches 6;
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Best Local Similarity 50.6%; Pred. No. 4.8e-07;
Matches 39; Conservative 0; Mismatches 6
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Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 45.3%
Matches 39; Conservative
                              APPLICANT: Gad, Alexander
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                                                                                                              APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
WHAPPER FILING DATE: 1999-09-24
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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 06/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3
LENGTH: 56
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKY-KAEAAKAAAKEAAYEA 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 64.8%; Score 138; DB 9; Length 109; Best Local Similarity 76.6%; Pred. No. 1.2e-07; Matches 36; Conservative 0; Mismatches 7; Indels
                        Sequence 7, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
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Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
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Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
US-09-816-989A-7
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US-09-816-989A-3
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US-09-816-989A-5
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPCLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/609/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: FOT/US99/22402
PRIOR APPLICATION NUMBER: PT/US99/224
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55748
LENGTH: 428
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                                                                                                                                                                                                                                                                                                                                                                                                                              50.9%; Score 108.5; DB 15; Length 428; 60.4%; Pred. No. 0.00079; ive 2; Mismatches 8; Indels 11;
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64.4%; Pred. No. 6.1e-05;
tive 1; Mismatches 5
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Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09816989A, Patent No. US20020115103A1; GENERAL INFORMATION:
                                                                                                                                                                                                                          TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-10-282-122A-55748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Manone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Maselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                              32; Conservative
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Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 32; Conserv
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US-09-816-989A-1
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                Query Match
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                                                          Sequence 4, Application US/09816989A

Sequence 4, Application US/09816989A

Patent No. US20020115103A1

GENERAL INFORMATION:
APPLICANT: Gad, Alexander

APPLICANT: Lis, Doris

TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REFERENCE: 2609/60807-4-ET-US

CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT FILING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: E0/101,693

PRIOR PILING DATE: 1998-09-25

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1

SOFTWARE: Patentin Version 3.1
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/201,078

PRIOR FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-24

PRIOR PILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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1 Similarity 71.1%; Pred. No. 5.4e-06; 
32; Conservative 0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 55748, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Majone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyekind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-55748
                              RESULT 6
US-09-816-989A-4
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; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-282-122A-59321
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Ohlsen, Kari
Syskind, Uudith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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52.9%;
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                  FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 52.9*
Matches 27; Conservative
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/201,078
FRIOR PILING DATE: 2000-03-21
FRIOR PILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-06
FRIOR PRIOR FILING DATE: 2000-09-06
FRIOR FILING DATE: 2000-09-05
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-110-23
FRIOR FILING DATE: 2000-110-23
FRIOR FILING DATE: 2000-110-29
FRIOR FILING DATE: 2000-110-20
FRIOR FILING DATE: 2000-110-20
FRIOR FILING DATE: 2001-10-20
FRIOR FILING DATE: 2001-10-20
FRIOR FILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-03-09
FRIOR FILING DATE: 2001-03-09
FRIOR FILING DATE: 2001-03-09
FRIOR FILING DATE: 2001-
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION UNBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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Best Local Similarity 65.3%; Pred. No. 0.011;
Matches 32; Conservative 2; Mismatches 9; Indels
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PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-66
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-03-06
PRIOR PLILNG DATE: 2000-03-06
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ollsen, Kari
APPLICANT: Ollsen, Kari
APPLICANT: Yiskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ), ORGANISM: Escherichia coli
US-10-282-122A-56483
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US-10-282-122A-59321
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APPLICANT: AU, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PLICATION NUMBER: 60/242,578
PRIOR PELING DATE: 2000-10-23
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-112-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-03
PRIOR PLING DATE: 2001-02-03
PRIOR PLING DATE: 2001-02-04
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-
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Pred. No. 0.017;
4; Mismatches 14; Indels
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TITLE OF INVENTION: Diagnosis, Prevention and Treatment of Ulcerative Colitis, and Clinical Subtypes Thereof, Using Microbial UC pANCA antigens
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                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/229,567

FILING DATE: 27-Aug-2002

CLASSIFICATION: VUNKnown>
PRIOR APPLICATION: VUNKnown>
PRIOR APPLICATION NUMBER: US/09/417,264

FILING DATE: CUNKnown>
APPLICATION NUMBER: US 09/041,889

FILING DATE: CUNKnown>
APPLICATION NUMBER: US 09/041,889

FILING DATE: CALRYIN A.

RAME: CAMPALION: ACHAYN A.

REFERENCE/DOCKET NUMBER: P-PM 3006

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
Best Local Similarity 59.6%; Pred. No. 0.03; Matches 28; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 62547, Application US/10282122A; Publication No. US20040029129A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                               Sequence 27, Application US/10229567
Publication No. US20030092080A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Braun, Jonathan
Cohavy, Offer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 27
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 55.6
nes 25; Conservative
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US-10-229-567-27
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Matches
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Publication No. US2020197265A1

GENERAL INFORMATION:
APPLICANT: Wateson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REFERENCE: 11000.10062
FILE REFERENCE: 11000.10062
CURRENT APPLICATION NUMBER: US/10/051,643
FRICR FILING DATE: 2002-01-18
FRICR FILING DATE: 1998-09-17
FRICR APPLICATION NUMBER: US 09/156,181
FRICR FILING DATE: 1998-09-17
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; Sequence 52, Application US/10205979
; Publication No. US20030147861A1
; GENERAL INFORMATION:
; APPLICANT: Wateon, James D.
; APPLICANT: Abernethy, Nevin
; TITLE OF INVENTION: Of Immune Responses
; FILE REFERENCE: 11000.1063U
; CURRENT APPLICATION NUMBER: US/10/205,979
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,446
; NUMBER OF SEQ ID NOS: 52
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                       Score 94.5; DB 15; Length 239;
Pred. No. 0.014;
7; Mismatches 9; Indels 5
                                                                                                                                                                                                                                                                                                1 AKKYA-KKAKAEKAKKAYKAAEAKKAAKYEKAA-AEKAAAKEAAYEA 45
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Pred. No. 0.03;
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                                                                                                                                      44.4%; Sco. No. v. 56.2%; Pred. No. v. 7; Mismatches
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                                                 TYPE: PRT
ORGANISM: Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-205-979-52
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                                                                                                                                                                                                              27; Conservative
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Best Local Similarity
                                                                                                                                                                                  Local Similarity
                                                                                     ; OKGHNISH: LLCC.--US-10-282-122A-60543
SEQ ID NO 60543
LENGTH: 239
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US-10-051-643-201
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LENGTH: 223
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                                                                                                                                                            Query Match
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APPLICANT: Trawick, John
APPLICANT: Trawick, Mohert
APPLICANT: Xu, H.
FUERENESCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: 60,120,202,022
CURRENT APPLICATION NUMBER: 60,120,038
FRIOR PELING DATE: 2000-03-23
FRIOR PELING DATE: 2000-05-23
FRIOR PELING DATE: 2000-05-23
FRIOR PELING DATE: 2000-05-24
FRIOR PELING DATE: 2000-05-26
FRIOR PELING DATE: 2000-01-23
FRIOR PELING DATE: 2000-01-23
FRIOR PELING DATE: 2000-11-27
FRIOR PELING DATE: 2000-11-27
FRIOR PELING DATE: 2000-11-27
FRIOR PELING DATE: 2000-12-3
FRIOR PELING DATE: 2000-12-3
FRIOR PELING DATE: 2001-02-09
FRIOR PELIN
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ORGANISM: Mycobacterium bovis
                                            Ohleen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
Haselbeck, Robert
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Search completed: December 14, 2004, 06:59:40 Job time: 111.646 secs

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LENGTH: 45
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Sequence 7, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 201, Appl
Sequence 201, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 2699, A
Sequence 18922, A
                                                                             December 14, 2004, 05:47:53 ; Search time 12.6266 Seconds (without alignments) 236.351 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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                                                                                                                                                            1 AKKYAKKAKAEKAKKAYKAA......AKYEKAAAEKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-405-743A-7

US-09-405-743A-3

US-09-405-743A-6

US-09-405-743A-6

US-09-405-743A-1

US-09-405-743A-1

US-09-405-743A-1

US-09-405-743A-1

US-09-405-743A-1

US-09-405-743A-1

US-09-405-743A-1

US-09-011-899-27

US-09-225-991A-25-891

US-09-225-991A-25-891

US-09-134-000C-5990

US-09-134-000C-5990

US-09-134-000C-5990

US-09-134-000C-5990

US-09-107-532A-5094

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US-09-417-264-39

US-09-417-264-39
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S-09-041-889-38
S-09-417-264-38
S-09-041-889-40
S-09-417-264-40
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                                                                                                                                                                                                                              478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                     - protein search, using sw model
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213
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77.5
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131
126.5
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89.5
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                                                     OM protein
                                                                                                                                                                                                                                                                                    Minimum DB
Maximum DB
                                                                                                                                                              Sequence:
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                                                                              Run on:
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No.
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                     13743, A
15, Appl
39148, A
4836, Ap
4840, Ap
2, Appli
5390, Ap
33, Appli
33, Appli
32, Appli
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16, Appl
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                                                                                                        Sequence
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GENERAL SCREATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
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GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS FILE REPERBNCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 109
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100.0%; Score 213; DB 4; Length 45;
1 Similarity 100.0%; Pred. No. 1.8e-16;
45; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
FEBATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: PEPTIDE
US-09-405-743A-7
                    US-09-489-039A-13743
US-09-247-054-15
US-09-247-054-15
US-09-270-767-543168
US-09-213-999C-4836
US-09-923-304-2
US-09-923-304-2
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US-09-543-999C-4839
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US-08-513-055-13
US-08-154-141-32
US-08-154-133
US-08-154-133
US-08-154-133
US-08-154-133
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US-08-154-133
US-08-154-133
US-08-177-304-13
             -09-417-264-32
-09-489-039A-13743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
 222
222
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Best Local Similarity
Matches 45; Conserva
 US-09-405-743A-2
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RESULT 5
US-09-405-743A-6
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                                          Gaps
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APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                          Sequence 3, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Veda Research and Development Co., Ltd.
APPLICANT: GEAR RESEARCH and DEVELORMEN WEIGHT WARKERS;
ITTLE OF INVENTION: GLATTRAMER ACETATE MOLECULAR WEIGHT MARKERS;
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels 13;
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                                                                                                      65 AKKYAKAAKAE--KKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 63.1%; Score 134.5; DB 4; Length 56; Best Local Similarity 68.4%; Pred. No. 5.3e-08; Matches 39; Conservative 0; Mismatches 5; Indels 1
64.8%; Score 138; DB 4; Length 109; 76.6%; Pred. No. 4.4e-08; ive 0; Mismatches 7; Indels
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Pred. No. 1.7e-07;
0; Mismatches 6; Indels
                                                                              ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-5
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50.6%;
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Best Local Similarity 50.6'
Matches 39; Conservative
                                      36; Conservative
                      Local Similarity
                                                                                                                                                                          RESULT 3
US-09-405-743A-3
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US-09-405-743A-5
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LENGTH: 56
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LENGTH: 77
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    Query Match
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                      Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       SYNTHETIC
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Patent No. 6514938
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Veda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT APPLICATION NUMBER: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
LENGTH: 66
                                              GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Yeda Research and Development Co., Ltd.

TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS

TITLE OF INVENTION: G.007-4

CURRENT APPLICATION UNMBER: US/09/405,743A

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 86
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Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 AKKYAKAKAE--KKEYAAEAK----YKAEAAKAAKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: DESCRIPTION of Artificial Sequence:
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 120.5; DB 4;
Pred. No. 1.9e-06;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
59.4%; Score 126.5; DB 4
Best Local Similarity 45.3%; Pred. No. 5.8e-07;
Matches 39; Conservative 0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YKAEAAKKAYKAEAAKAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 ------KAAAEKAAAKEAAYEA 45
Sequence 6, Application US/09405743A Patent No. 6514938
                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 71.1%;
Matches 32; Conservative
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ORGANISM: Artificial Sequence
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APPLICANT: Wateon, James D.
APPLICANT: Wateon, James D.
APPLICANT: Tan. Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
FILE REPERENCE: 11000.1002c4
CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER FILING DATE: 1998-06-11
EARLIER FILING DATE: 1998-06-12
EARLIER FILING DATE: 1997-06-12
EARLIER FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 42.7%; Score 91; DB 3; Length 223; Best Local Similarity 59.6%; Pred. No. 0.0095; Matches 28; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 42.7%; Score 91; DB 4; Length 223; Best Local Similarity 59.6%; Pred. No. 0.0095; Matches 28; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYA-KKAKAEKAKKAYKAAEAKKAAKYEKAA-AEKAAAKEAAYEA
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SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                 11000.1002c3
                                                                         US/09/095,855
                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,347
FILING DATE: 29-40G-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 201, Application US/09205426 Patent No. 6406704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 223 amino acids
                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                  FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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US-09-205-426-201
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Sequence 13656, Application US/09489039A

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489, 039A
CURRENT APPLICATION NUMBER: US/09/489, 039A
PRIOR APPLICATION NUMBER: US/06/117,747
PRIOR FILING DATE: 1999-01-29
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Patent No. 6160093

GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                            SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 AAEAQKKAEAAAAKKAQGEAEKKAQQEAAKQAAABKAAABKAAABKAAAQKA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                                                                                                                                                                                                        50.7%; Score 108; DB 4; Length 35;
64.4%; Pred. No. 2.2e-05;
tive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKEKA--AKKAYK------KEAKAKAABAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKAKAKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
CURRENT APPLICATION NUMBER: US/09/405,743A CURRENT FILING DATE: 1939-09-24 WUWBER OF SEQ ID NOS: 7.2.1 SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Klebsiella pneumoniae
                                                                                                SEQ ID NO 1
LENGTH: 35
TYPE: PR
ORGANISM: Artificial Sequence
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COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13565
LENGTH: 469
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 64.4
Matches 29; Conservative
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nes 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-09-489-039A-13565
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US-09-095-855-201
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Matches
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Sequence 26999, Application US/09248796A

Sequence 26999, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Keith Meinstock et al

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REPERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

FRIOR PAPLICATION NUMBER: US 60/074,725

PRIOR PAPLICATION NUMBER: US 60/096,409

PRIOR PELING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 26989

LENGTH: 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.0%; Score 89.5; DB 4; Length 214; 55.6%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.4%; Score 86; DB 4; Length 148; 48.9%; Pred. No. 0.021; tive 10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKAKAKKAYKAABAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AKKKAEEAKKKEEEAKKAEEAKKAEEAKKVEEAAKKAEEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-092-252-991A-29581
; Sequence 29581, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                 P-PM 3006
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/041,889
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-PM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 214 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Candida albicans
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Best Local Similarity 48.9%
Matches 23; Conservative
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Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-248-796A-26989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-417-264-27
    COUNTRY:
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APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC pANCA antigens
TITLE OF INVENTION: Microbial UC pANCA antigens
NOMBER OF SEQUENCES: 41
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                      Diagnosis, Prevention and Treatment of
Ulcerative Colitis, and Clinical Subtypes Thereof, Using
Microbial UC pANCA antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 0.013;
4; Mismatches 13; Indels
137 AKKAATKAAPAKKATAAKKAAPAKKATAAKKAAPAKKAPAKKAATKA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                                                                                                                                                   E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-PM 3006
TELECHONINICATION INFORMATION:
TELEPAN: (619) 535-8949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 27, Application US/09417264
; Patent No. 6537768
; GENERAL INFORMATION:
                                                                                                          Sequence 27, Application US/09041889
Patent No. 6033864
                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis
TITLE OF INVENTION: Ulceratis
TITLE OF INVENTION: Microbial
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.6%
Them 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-889-27
                                                                                                                                                                                                                                                                                                                                                       LITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       San Diego
California
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                              RESULT 11
US-09-041-889-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-417-264-27
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Sequence 18922, Application US/09248796A

Sequence 18922, Application US/09248796A

Sequence 18922, Application US/09248796A

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: 107196, 132

CURRENT APPLICATION NUMBER: US/09/248, 796A

CURRENT FILING DATE: 1999-02-12

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 18922
               APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-03-18
PRIOR FILING DATE: 1998-03-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.9%; Score 85; DB 4; Length 176; 50.0%; Pred. No. 0.033; tive 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
40.4%; Score 86; DB 4; Length 407;
Best Local Similarity 51.1%; Pred. No. 0.06;
Matches 24; Conservative 6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-18922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 50.0
Matches 27; Conservative
GENERAL INFORMATION:
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Search completed: December 14, 2004, 05:50:16 Job time : 13.7694 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 14, 2004, 05:47:53 ; Search time 12.8776 Seconds (without alignments) 418.411 Million cell updates/sec Run on:

US-10-792-311-3 266 1 AKKYAKKEKAYAKKABKAAK......BAKYKABAAKAAAKBAAYEA 56 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

RESULT 2 AE1317

histone H1-delta -	histone H1 (clone	histone H1-II - Vo	conserved hypothet	IgA-specific metal	histone H1 - Chlam	immediate-early pr	translation initia	probable late embr	histone H1 - trout	tolA protein VC183	arylesterase-relat	hypothetical prote	hypothetical prote	histone H1 (clone	hypothetical prote
A32137	T06241	JN0748	E75383	A26039	SS9589	EDBEQ3	AI0424	T14305	HSTR1	A82152	G87675	T32633	T34010	T06257	T03561
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185	284	241	581	1532	231	407	884	136	194	356	438	1655	1482	288	461
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34	34	34	34	34	33	33	33	33	33	33	33	33	33	33	33
91.5	91.5	91	90.5	90.5	90	90	90	89.5	89.5	89.5	89.5	89	88.5	88	88
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1	
	10005/ told protein - Escherichia coli (strain K-12)	
	C:Specise: Becnerichia coli C:Date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text change 09-Jul-2004	
	C; Accession: JV0057; B64810	
	R;Levengood, S.K.; Webster, R.E. J. Bacteriol. 171, 6600-6609, 1989	
	A; Title: Nucleotide sequences of the tolA and tolB genes and localization of their produc	eir produc
	A; Kretzferde Inducer: UVO05/; MOID: 900/0104; FMID: 200/24/ A; Accession: UV0057	
	A; Molecule type: DNA A:Readdhes: 1-421 < LRV>	
	A; Cross-references: UNIPROT: P19934; GB: M28232; NID: g148018; PIDN: AAA24683.1; PID: g148019	D:g148019
	A; Experimental source: strain JM105 A:Note: the authors translated the initiation codon GTG for residue 1 as Val	
	R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley	y, M.; Co]
	.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997	
	A,Title: The complete genome sequence of Escherichia coli K-12.	
	A;Reference number: A64720; MUID:97426617; PMID:9278503 A:Accession: R64810	
	A. Status: nucleic acid sequence not shown: translation not shown	
	A; Molecule type: DNA	
	A;Residues: 1-421 <blat></blat>	
•	A; Cross-references: GB: AE000177; GB: U00006; NID; 91786965; PIDN: AAC73833.1; PID: 91786960;	91786960;
	Ajasperimental Bource: Surfain N-12, Bubberain Majos C.Comment: folk and folk broteins are necessary for colicins E2, E3, A, and K to reach the	o reach th
	C,Genetics:	
	A;Gene: tolA	
	A; Map position: 17 min	
	Assart codon: GTG	
	C;Keywords: nucleotide binding; P-loop; transmembrane protein F:14-34/Domain: transmembrane #status breditted <mss< th=""><th></th></mss<>	
	F;78-301/Domain: helical #status predicted <hsr></hsr>	
	F;355-562/Region: nucleoride-binding morth A (F-100p)	
	44.08;	
	Best Local Similarity 54.7%; Pred. No. 0.0048; Matches 35; Conservative 5; Mismatches 10; Indels 14; Gaps 2;	
	Qy 7 KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEA 52	
• •	:	
	Oy 53 AYEA 56	
	Db 208 RKKA 211	

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A;Cross-references: UNIPROT:Q8X965; GB:AE005174; NID:g12513672; PIDN:AAG55075.1; GSPDB:GR
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: tolA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CiSpecies: Salmonella enterica subsp. enterica serovar Typhi (strain CT18) (Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi (Spacies) has also been called Salmonella typhi (Spacesion: AG0592 (MUD):21534947; PMID:11677608 (Spacesion: AG0592 (MUD):21534947; PMID:11677608 (Spacesion: AG0592 (MUD):21534947; PMID:11677608 (Spacesion: AG0592 (Spa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C)Accession: T09127
R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
Proc. Natl. Acad. Sci. U.S.A. 95, 1230-1235, 1398
A;Title: A family of chimeric erythrocyte binding proteins of malaria parasites.
A;Reference number: 216577; MUID: 98115903; PMID: 9448314
A;Accession: T09127
A;Accession: T09127
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1701 cKAP>
A;Esidues: 1-1701 cKAP>
A;Esidues: 1-1701 cKAP>
A;Esperimental source: subspecies yoelii; strain YM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule fype: DNA
A;Residues: 1-376 <PAR>
A;Residues: 1-376 <PAR>
A;Croser-references: GB:AL513382; PIDN:CAD05209.1; PID:g16501979; GSPDB:GN00176
C;Genetics:
A;Gene: STY0793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable erythrocyte-binding protein MAEBL - Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------KYKAEAAKAA
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 EKAYAKKAEKAAKKAEAKAYK-AAEAKKKAEA-----KYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 62/1; 1648/1; 1674/2; 1697/1
C;Keywords: alternative splicing; cell binding; erythrocyte invasion
                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 376;
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                                                                                                                                                                                                                                                                               Length 394;
                                                                                                                                                                                                                                                                                                                                                              11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.4%; Score 110; DB 2; 54.2%; Pred. No. 0.054;
                                                                                                                                                                                                                                                                       Query Match
42.5%; Score 113; DB 2;
Best Local Similarity 60.0%; Pred. No. 0.0098;
Matches 33; Conservative 5; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 ADAKKKADAEA 211
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Gene: maebl
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AG0592
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hypothetical protein Imc1941 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
E;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: ABI317
B;Glaser. P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
J; Dominguez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A,Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Macok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A,Title: Comparative genomics of Listeria species.
A,Title: Comparative genomics of Listeria species.
A,Feference number: ABI377
A,Status: preliminary
A,Reference number: ABI377
A,Status: preliminary
A,References: UNIPROT:Q8YSW4; GB:NC_003210; PIDN:CAD00019.1; PID:g164111394; GSPDB: A,Generics:
C;Generics: M;Gene: Imo1941
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC80774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
(885576
membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G85576
B;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew alure 409, 529-533, 2001
A;Ature 409, 529-533, 2001
A;Ature 409, 529-533, 2001
A;Atle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A88480; MUD:21074935; PMID:11206551
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ω.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Escherichia coli
C;Date: 18-701-2001 #sequence_revision 18-701-2001 #text_change 09-701-2004
C;Accession: P90725
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Ogasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-394 <HAX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 EKAYAKKAEKAAKKAEAKAYK-AAEAKKKAEA----KYKAEAAKAAAKEAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
43.8%; Score 116.5; DB 2; Length 239;
Best Local Similarity 55.4%; Pred. No. 0.0034;
Matches 31; Conservative 9; Mismatches 15; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.5%; Score 113; DB 2; Length 394;
60.0%; Pred. No. 0.0098;
ive 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 60.0
Matches 33; Conservative
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C;Accession: E83525
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc A;Reference number: A82950; MUID: 20437337; PMID: 10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004
C;Accession: A28100
R;Lai, Z.C.; Childs, G.
Mol. cell. Biol. 8, 1842-1844, 1988
A;Title: Characterization of the structure and transcriptional patterns of the gene encoda;Reference number: A28100; MUID:88246461; PMID:2837660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: UNIPROT:P50600; GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG0436(
A,Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 histone H1-beta, embryonic - sea urchin (Strongylocentrotus purpuratus)
                                                                                                                                                                                                             Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A28100
A;Molecule type: DNA
A;Residues: 1-211 <LAI>
A;Cross-references: UNIPROT:P15869; GB:M20314
C;Superfamily: histome H1
C;Keywords: chromosomal protein; DNA binding; embryo; nucleosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.5%; Score 102.5; DB 2; 43.0%; Pred. No. 0.067; ive 7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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Pred. No. 0.05;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKKAEKAAKKAEAKA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 KKKA--EAKYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.3%;
                                                                               156 PAKKAAKKPAAKKA 169
                                                                                                                                                                                                       Tola protein PA0971 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 43.0 Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                           43 EAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | || :|
KPAAKKA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-347 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 KEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: E83525
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: tolA; PA0971
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Best Local S:
Matches 30
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                                                                                                                                                                                                                                                   C;Species: Heemophilus influenzae
C;Species: Heemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Species: Heemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: G4064; JG5212
B;Feleschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.D.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Accession: G64064
A;Accession: G64064
A;Accession: G64064
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-372 <TIGRS
A;Cross-references: UNIPROT: P44678; GB:U32722; GB:L42023; NID:g1573348; PIDN:AAC22041.1;
B;Sen, K.; Sikkema, D.J.; Murphy, T.F.
Gene 178, 75-81, 1996
A;Title: Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA a;A;Reference number: JG5212; MUD:97080550; PMID:8921895
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Residues: 'V',2-47,'A',49-141,'R',143-164,'P',166-189,'R',191-202,'A',204-226,'A',228-
:Cross-references: GB:U32470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A25550
histone H1 - sea urchin (Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A25550
R;Knowles, J.A.; Childs, G.J.
Nucleic Acids Res. 14, 8121-813, 1986
A;Fitle: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus A;Reference number: A2550; MUID:87040778; PMID:3022245
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Cross-references: UNIPROT:P06144; GB:X04488; NID:g9616; PIDN:CAA28177.1; PID:g9617; Superfamily: histone H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ï
                                                                                                                                                                                                                                      outer membrane integrity protein tolA - Haemophilus influenzae (strain Rd KW20)
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                                                      26
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     Gaps
                                                    5 AKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEA-----KYKAEAAKAAAKEAAYEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.7%; Score 105.5; DB 2; Length 372; 48.2%; Pred. No. 0.04; ive 14; Mismatches 14; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 210;
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C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
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  14; Indels
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  Mismatches
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Conservative
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Best Local Similarity
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A;Start codon: GTG
32;
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ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Status: preliminary
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Residues: 1-243 <GLA>
A;Cross-references: UNIPROT:092A67; GB:AL592022; PIDN:CAC97285.1; PID:g16414556; GSPDB:GRA;Sperimental source: strain Clip11262
C;Genetics:
A;Gene: lin2055
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C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C.Date: 109-Martin, S.R.; Thomas, J.O.
EMBO J. 8, 2591-2599, 1989
A.Thill: C.S.; Martin, S.R.; Thomas, J.O.
A.Reference number: S09388; MUID:90060019; PMID:2583125
A.Recession: S09388
A.Reference number: S09388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KKYAKKEKAYAK-----KAEKAAKKAEAKAYKAAEAKK----KAEAKYKAEAAKAAAK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein A208R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAE-AKYKAEAAKAAAKEAAYE 55
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 37.0%; Score 98.5; DB 2; Length 243; Best Local Similarity 50.0%; Pred. No. 0.11; Matches 28; Conservative 9; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 311;
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43.9%; Pred. No. 0.13;
tive 8; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 97.5; DB 2;
Pred. No. 0.12;
3; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-311 <GRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        histone H1 - sea urchin (Parechinus angulosus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Accession: T17698
R,Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A,Reference number: Z18806
A,Accession: T17698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q7M409
C;Superfamily: histone H1
C;Keywords: chromosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.6%;
Matches 30; Conservative
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Matches 29; Conservative
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A21689
hypothetical protein homolog lin2055 [imported] - Listeria innocua (strain Clip11262)
c;Species: Listeria innocua
c;Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1689
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
R;Glaser, P.; Frangeul, L.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A02584
A;Molecule type: DNA
A;Residues: 1-206 AMEZ>
A;Cross-references: UNIPROT:P06350; GB:X02624; NID:g64323; PIDN:CAB37646.1; PID:g4468016
C;Superfamily: histone H1
C;Superfamily: histone H1
F;Reywords: chromosomal protein; DNA binding; nucleosome
F;1-44/Region: flexible nose
F;45-117/Region: globular head
                C;Species: Drosophila hydei
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accessins 551364; 834154
C;Accessin J.; Padmanabhan, 8.; Buenemann, H.
Eur. J. Biochem. 225, 1089-1095, 1994
Eur. J. Biochem. 225, 1089-1095, 1994
Eur. J. Biochem. 226, 1089-1095, 1994
Eur. J. Biochem. 226, 1089-1095, 1994
Eur. J. Biochem. 225, 1089-1095, 1994
Eur. J. Biochem. 251364; MUID:95045538; PMID:7957199
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C;Species: Oncorhynchus mykiss (rainbow trout)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Species: A02584
R;Mezquita, J; Connor W; Winkfein, R.J; Dixon, G.H.
J. Mol. Evol. 21, 209-229, 1985
A;Fitle: An HI histore gene from rainbow trout (Salmo gairdheril).
A;Reference number: A02584; MUID:85264847; PMID:6443128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKAYAKKAEK-----AAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAA
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                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: UNIPROT: Q08696; EMBL: X73481
R; Weesen, J; Heinleln, U.A.O.; Buenemann, H.
submitted to the EMBL Data Library, June 1993
A; Reference number: S34153
A; Reference number: S34154
A; Molecule type: DNA
A; Residues: 1-163, E', 164-236, 'Q', 237-254, 257-320, 'E', 321-1390 < NEW>
A; Cross-references: EMBL: X73481; NID: 9313201; PID: 9313202
C; Genetics: mst101(2)
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46.7%; Pred. No. 0.08;
tive 7; Mismatches 18; Indels
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Pred. No. 0.29;
5; Mismatches 18;
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A;Status: nucleic acid sequence not shown A;Molecule type: DNA
A;Residues: 1-1390 <NEE>
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les 28; Conservative
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Search completed: December 14, 2004, 05:52:13 Job time : 13.8776 secs

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Q9u762 aedes albop
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- 2004 Compugen Ltd.
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Q7RC08
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Q813A1
Q9RJT1
Q7W477
Q937K4
Q937K4
Q937K4
CAE80819
Q8XQ16
Q7AG18
Q8XQ16
Q7AG18
Q8XQ16
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Q8XQ16
Q7AG18
Q8XQ17
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Copyright (c) 1993
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1: uniprot_sprot:*
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39.5 436 2 39.3 346 1 39.3 1817 2 39.3 1817 2 39.3 1817 2 39.3 1830 2 39.3 1866 2 39.3 1866 2 38.7 441 2 38.7 1268 2 38.5 210 1 38.5 345 2 38.5 345 2		NULLY INTERVENCE PRELIMINARY; PRT; OTHERS ON TYENBLYER SEGUENCE FROM N.A. STRANN-RBSO ATCENDAGE SEGUENCE FROM N.A. SEGUENCE S	44.7%; Similarity 53.3%; 2; Conservative	akkyakkekayakka : : avekaaaekaaaekaae	PRELIMINARY;
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GO, GO:0016020; C:membrane; IEA.
GO, GO:0016020; C:mucleosome; IEA.
GO, GO:0005634; C:nucleosome; IEA.
GO, GO:0005634; C:nucleosome; IEA.
GO; GO:0005634; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006855; F:protein transporter activity; IEA.
GO; GO:0006856; F:protein transport; IEA.
GO; GO:0006819; P:nucleosome assembly; IEA.
GO; GO:0006819; P:nucleosome assembly; IEA.
InterPro; IPR00528; TolA.
InterPro; IPR005260; TolA.
InterPro; IPR005260; TolA.
InterPro; IPR005260; TolA.
                                                                                                                                                 MEDLINE=22433060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
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BENBL; AE006136; AAK03052.1; -. BENBL; AE00196; IGMJ.

InterPro; IPR009148; SibA.

InterPro; IPR010553; Tropomyosin.

Profest, PF06519; TolA; 1.
Bacteria, Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4.799-808(2002).
EMBL; AR016778, AAN66845.1; -.
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66.0%; Pred. No. 0.034;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pasteurella multocida.
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TIGRFAMS; TIGR01352; tonB_Cterm; 1.
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MEDLINE=21145866; PubMed=11248100;
                              Pseudomonadaceae; Pseudomonas NCBI TaxID=160488;
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Best Local Similarity 66.0
Matches 31; Conservative
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TIGR; PP1221; -.
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GO; GO:000786; C:mucleosome; IEA.
GO; GO:0005634; C:nucleosome; IEA.
GO; GO:0005634; C:nucleosome gace (sensu Gram-negative Bact. . .; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0005634; P:nucleosome assembly; IEA.
GO; GO:0015031; P:protein transporter activity; IEA.
GO; GO:0015031; P:protein transport; IEA.
InterPro; IPR010528; TolA.
InterPro; IPR010528; TolA.
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96198174; PubMed=8626299; Rodriguez-Herva J.J., Ramos J.; Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.; The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity of the cell envelope.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rodriguez-Herva J.J., Ramos J.; "Characterization of an OprL null mutant of Pseudomonas putida."; J. Bacteriol. 178:5836-5840(1996).
                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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66.0%; Pred. No. 0.034;
ive 2; Mismatches 12; Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; X74218; CABS0780.1; -.
HSSP; P50600; 1LR0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ramos-Gonzalez I.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
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                           Created)
Last sequence update)
Last annotation update)
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Bacteriol. 178:1699-1706(1996)
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                       01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2004 (TrEMBLrel. 26,
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=K12 / JM105;
MEDLINE=90078104; PubMed=2687247;
MEDLINE=90078104; PubMed=2687247;
Levengood S.K., Webster R.E.;
"Nucleotide sequences of the tolA and tolB genes and localization of their products, components of a multistep translocation system in Escherichia coli.";
J. Bacteriol. 171:6600-6609(1989).
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"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                            Gaps
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STRAIN=KIZ / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
MELLINE F. R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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MEDLINE=97133271; PubMed=8978668;
Derouiche R., Gavioli M., Benedetti H., Prilipov A., Lazdunski C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Levengood S.K., Beyer W.F. Jr., Webster R.E.;
"TOLA: a membrane protein involved in colicin uptake contains an
extended helical region.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=colA; Synonyms=cim, excC, lky; OrderedLocusNames=b0739; Escherichia coli.
                                                                                              44.0%; Score 117; DB 2; Length 389; 55.9%; Pred. No. 0.036; ive 7; Mismatches 15; Indels
                                                            389 AA; 42197 MW; B4032F2A2FD9E94B CRC64;
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                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                         421 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae, Escherichia.
PRINTS; PRO1852; SIBAPROTEIN.
PRINTS; PRO0194; TROPOMYOSIN.
Complete proteome.
SEQUENCE 389 AA; 42197 MW;
                                                                             Query Match
Best Local Similarity 55.2.
Best Annual Similarity
The 33; Conservative
                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                              TolA protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK--AAEAKKKAEAKYKAEAAKAAAKEAAYEA 56
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                 Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L., Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C., "Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";

Mat. Biotechnol. 22:55-61(2004).

EMBL, BAS72603; CAR226621.1; -.

InterPro; IPR05819; Histone_H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Larimer F.W., Chain P., Hauser L., Lamerdin J., Malfatti S., Do L., Lanid M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C., Harxison F.H., Gibson J., Harwood C.S.;

"Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";

Nat. Biotechnol. 22:55-61(2004).

EMBL, BX572603; CAE28621.1;
                                                                                                                                                                                                                                                                                                                            Query Match
43.4%; Score 115.5; DB 2; Length 105;
Best Local Similarity 58.6%; Pred. No. 0.016;
Matches 34; Conservative 4; Mismatches 17; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 43.4%; Score 115.5; DB 2; Length 105; Local Similarity 58.6%; Pred. No. 0.016; es 34; Conservative 4; Mismatches 17; Indels 3
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBL TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
NCBI_TaxID=1076;
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Hypothetical protein.
CEDB59B3D937E980 CRC64;
CEOHIENCE 105 AA; 11042 MW; CEDB59B3D937E980 CRC64;
                                                                                                                                                                                                                                                            Complete proteome; Hypothetical protein.
SEQUENCE 105 AA; 11042 MW; CEDB59B3D937E980 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1701 AA
PubMed=14704707; DOI=10.1038/nbt923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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SEQUENCE FROM N.A.
STORAGOS / ATCC BAA-98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                        PRINTS; PR00624; HISTONEHS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
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PubMed=14704707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAE28621;
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CAE28621
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                        7 KEKAYAKKAEKAAKKAEAKAYK-----AAEAKKKAEA-----KYKAEAAKAAAKEA 52
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAINE-2153729; PubMed=1679669;

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve B., de Daruvar A., Dusaurget O.,

Charbit C., Goebel W., Gomez-Lopez N., Hauf J., Dusaurget O.,

A Gautier L., Goebel W., Kaerte J., Kuhn M., Kunst F., Kurapkat G.,

Jones L.-M., Kaerset U., Krett J., Kuhn M., Kunst F., Kurapkat G.,

A Jones L.-M., Schlueter T., Simoes N., Tierrez A.,

Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

A vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

Comparative genomics of Listeria species.";

Science 294:849-852(2001).

SERBL, ALSIJUSH, CADO0019.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AEKAAEEKKAAAAEKAEADKKKQEEDAVKAANAKKEQEAAEEKAAADKAAAEKAAAE 171
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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ListLinist; LMO1941; -.
ListLinist; LMO1994; -.
GO; GO: 0016998; P: cell wall catabolism; IEA.
InterPro; IPR002482; LysM.
Pfam; PF01476; LysM; 1.
SMART; SM00257; LysM; 1.
Complete proteome.
SEQUENCE 239 AA; 25836 MW; 72E59D576E0D7832 CRC64;
                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                               239 AA.
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Matches 31, Conservative
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STRAIN=CGA009 / ATCC BAA-98;
                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                                                                                                                                Lmo1941 protein.
OrderedLocusNames=lmo1941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
OrderedLocusNames=RPA3180;
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                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                Listeria monocytogenes.
                                                                                                                                          208 RKKA 211
                                                                                           53 AYEA 56
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RESULT 6
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09 Y5 W4
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47 AAAKEAAYEA 56
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Q8FJT1
                                                                                                                                                                    RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                     Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Shallom S.J., van Aken S.B., Riedmuller S.B., Eiddblyum T.V., Chackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Cunningham D.A., Preiser P.R., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., Carucci D.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.4%; Score 115.5; DB 2; Length 1701; 59.3%; Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary data.

EMBL, ABLO1001968; EAA18109.1; -. GO; GO:00104872; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR008602; Duffy binding.

Pfam; PF05424; Duffy binding.

SEQUENCE 1701 AA; 197910 MW; 03BE665BAE45C669 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Membrane spanning protein.
Name=tolA; OrderedLocusNames=S0571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22590274; PubMed=12704152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 59.3
hes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shigella flexneri.
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                                                                PubMed=12368865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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2072204
DO 707220
AC 077220
DT 05-JU
D
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8
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-----AAEAKKKAEA-----KYKAEAAK 46
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                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathogenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia. "NCBI_TaxID=217992;
                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.
                                                                                          01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MRA-2004 (TrEMBLrel. 26, Last annotation update)
Membrane spanning protein, required for outer membrane integrity.
Name=tolA, OrderedLocusNames=SF0558;
Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 43.2%; Score 115; DB 2; Length 41. Best Local Similarity 51.4%; Pred. No. 0.055; Matches 36; Conservative 5; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 AA; 42355 MW; 93E10F2C5DE60DE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
   413 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of uropathogenic Escherichia coli.";
                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TolA protein.
Name=tolA; OrderedLocusNames=c0818;
PRT;
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MEDLINE=22388234; PubMed=12471157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR010528; TolA. Pfam; PF06519; TolA; 1. Complete proteome. SEQUENCE 413 AA; 42355
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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9

Query Match

Matches

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Q7W477 Q7W477

RESULT 13

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McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Mayuen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Materston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKKAEKAA----KYAEAKAYK-AAEAKKKAEA------KYKAEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhimurium.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ray M.C., Vianney A., Cotte-pattat N., Lazzaroni J.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ297885, CAC62708.1; -.
HSSP; P19934, ITOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41601 MW; 3C0C1DC12E181013 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 AA; 41865 MW; 2534352116602D75 CRC64;
                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Last sequence update) U-MAR-2004 (TrEMBLrel. 26, Last annotation update) Tol protein, membrane spanning protein.
Name=tolA, OrderedLocusNames=STM0747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.0%; Score 114.5; DB 2;
54.2%; Pred. No. 0.058;
tive 11; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.7%; Score 113.5; DB 49.3%; Pred. No. 0.072;
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                                            395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407
                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae; Salmonella
                                                                                                 01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AE008730, AAL19691.1;
HSSP, P19934, 1TOL.
InterPro, IPR010528, TolA.
Pfam, PF06519; TolA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 AKAAA---KEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro; IPR010528; TolA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 49.3% les 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 54.2
hes 32; Conservative
                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 413:852-856(2001)
                                                                                                                                                                                                                                                     Erwinia chrysanthemi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF06519; TolA;
SEQUENCE 395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
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                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=556;
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                                                                                                                                                                                         Tola protein.
Name=tola;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Q8ZQT6;
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Matches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN=12822 / ATCC BAA-587;

STRAIN=12822 / ATCC BAA-587;

MEDLINE=22827954; Pubmed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; Pubmed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; Pubmed=12910271; DOI=10.1038/ng1227;

A Barkhill J., Sebalhia M., Temple L., James K.D., Harris B., Quail M.A., Achtman M., Atkin R., Baker S., Bancen K.D., Harris B., Quail M.A., Achtman M., Atkin R., Baker S., Bason N., Cherevach I., Achtman M., Atkin R., Baker S., Bason N., Cherevach I., Chillingworth T., Collin M., Cronin A., Davis P., Doggett J., Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Rabbinowitsch E., Rutter S., Sanders D., Seeger V., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Anthin L., Whitchead S., Barrell B.G., Maskell D.J., Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica.", Nat. Genet. 35:32-40(2003).

Remis. Bx640434; CAE39074.1; -. GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0015031; P:protein transporter activity; IEA.

InterPro; IPR016528; TonB.C.

Remis. PR06519 TonB.C.

Remis. PR06519 TonB.C.
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                                                                                                                                                                                                                                                                                                                                                                          7 KEKAYAKKAEKAA-----KKAEAKAYKAA-BAKKKAEA----KYKAEAAKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAYAKKA-EKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYE 55
                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella parapertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 43.0%; Score 114.5; DB 2; Length 373; 1 Similarity 55.4%; Pred. No. 0.055; 31; Conservative 8; Mismatches 16; Indels 1.
                                                                                                                                                                                                                                                  Score 115; DB 2; Length 421;
Pred. No. 0.056;
6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 AA; 40092 MW; A364894DAE46E328 CRC64;
                                                                                                                                                                                         DB296626F056D385 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002)
EMBL; AE016757; AAN79291.1; -.
HSSP; P19934; 1TOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sec
01-MAR-2004 (TrEMBLrel. 26, Last and
Proline-rich inner membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF06519; TolA; 1.
TIGRFAMS; TIGR01352; tonB_Cterm; 1.
                                                                                                                                                             Complete proteome.
SEQUENCE 421 AA; 43184 MW;
                                                                                                                                                                                                                                                     43.2%;
                                                                                                                                                                                                                                                                                  56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OrderedLocusNames=BPP3791;
                                                                                           InterPro; IPR010528; TolA.
Pfam; PF06519; TolA; 1.
                                                                                                                                                                                                                                                                               Local Similarity 56.2
Les 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 RKKA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 AYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete |
SEQUENCE
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26

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44

19;

Query Match

Matches

14

RESULT

셤

8

q

||||| |:| || 183 AKAAADAKKKAEAEA 197

Search completed: December 14, 2004, 06:10:16 Job time : 63.8523 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                 Copyright
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OM protein - protein search, using sw model

Run on:

December 14, 2004, 05:47:53 ; Search time 15.1772 Seconds (without alignments) 418.411 Million cell updates/sec

US-10-792-311-4

313 1 AKKYAKKEKAYAKAKKAEAK......BAKYKAEAAKAAAKEAAYEA Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	132.5	42.3	394	7	F90725	membrane spanning
7	132.5	42.3	394	7	G85576	membrane spanning
e	131	41.9	421	7	JV0057	tolA protein - Esc
4	123	39.3	248	Н	HSUR1P	histone H1, gonada
ß	122.5	39.1	376	~	AG0592	-
9	121.5	38.8	1390	~	S51364	sperm tail-specifi
7	119.5	38.2	347	~	E83525	Tola protein PA097
80	118	37.7	231	~	S59589	histone H1 - Chlam
0	117.5	37.5	372	~	G64064	outer membrane int
10	117	37.4	388	7	AC0138	Tola colicin impor
11	115.5	36.9	206	7	809388	histone H1 - sea u
12	115	36.7	344	0	834153	mst101-1 protein -
13	113	36.1	284	7	T06241	histone Hi (clone
14	112.5	35.9	217	0	A26721	histone H1-gamma,
15	112	35.8	243	~	AE1689	
16	111.5	35.6	239	0	AE1317	
17	111	35.5	210	~	A25550	histone H1 - sea u
18	110	35.1	220	N	A28456	histone H1.10 - ch
19	109	34.8	209	٦	HSXL1A	histone H1A - Afri
20	107	34.2	384	~	B43592	outer membrane pro
21	107	34.2	1701	7	T09127	probable erythrocy
22	106	33.9	214	~	G70673	probable hupB - My
23	105	33.5	211	7	A28100	histone H1-beta, e
24	104	33.2	311	7	T17698	hypothetical prote
25	103	32.9	182	~	S61926	histone H1 homolog
26	102.5	32.7	433	0	S25194	zuotin - yeast (Sa
27	102	32.6	924	7	T06636	hypothetical prote
28	101.5	32.4	236	7	S22322	histone H1 - wheat
29	101.5	32.4	1128	C3	T30296	R27-2 protein - Tr

histone H1 - rainb	translation initia	histone HlA - Afri	histone H1.11L - c	conserved hypothet	histone H1 - musco	histone H1-II - Vo	cytosolic repetiti	histone H1 (clone	tolA protein VC183	arylesterase-relat	histone H1.03 - ch	histone H1 - trout	histone H1B - Afri	histone HIB - Afri	histone H1.C - Afr
HSTR1R	E64114	151227	B28456	E75383	S01262	JN0748	A44993	T06257	A82152	G87675	D28456	HSTR1	HSXL1B	151447	833219
н	~	~	~	~	N	~	7	7	~	7	~	Н	Н	7	8
206	829	229	225	581	218	241	328	288	356	438	224	194	219	220	221
32.3	32.3	31.8	31.6	31.6	31.5	31.5	31.5	31.3	31.2	31.2	31.0	30.8	30.8	30.8	30.8
101	101	99.5	66	66	98.5	98.5	98.5	98	97.5	97.5	97	96.5	96.5	96.5	96.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	5

ALIGNMENTS

		Ø	
		(strain 0157:H7,	
		coli	
		Escherichia	
		ı	
		[imported]	
RESULT 1	F90725	membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, s	C;Species: Escherichia coli

substrain F

C, Date: 10-701-2004
C; Date: 10-701-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C; Accession: 90725
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G., gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: P90725
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-394 cHAX>
A; Residues: 1-394 cHAX>
A; Residues: 1-394 cHAX>
A; Residues: UNIPROT:Q8X965; GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GRA; B; Baperimental source: strain O157:H7, substrain RIMD 0509952

C,Genetics: A,Gene: EC80774

4 Gaps 9; Length 394; Indels ch 1 Similarity 58.9%; Pred. No. 0.0011; 43; Conservative 8; Mismatches 13; Query Match Best Local Similarity Matches 43; Conserva

54 1 AKKYAKKEKAYAKAKAEAKAAKKAKAEAKKYAKAA-----KAEKKEYAAAEAKYKAEA 음 ò

55 AKAAA-KEAAYEA 66 ð

|||| |:|| :| 214 EKAAADKKAAEKA 226 g

membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain F

C;Species: Bacherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: G85576 B;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-33, 2001 A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7. A;Accession: G85576 A;Accession: G85576 A;Status: preliminary A;Nolecule type: DNA A;Residues: 1-394 <STO>

A;Cross-references: UNIPROT;Q8X965; GB:AE005174; NID:g12513672; PIDN:AAG55075.1; GSPDB:GA A;Experimental source: strain 0157:H7, substrain EDL933 C;Genetics:

C;Genetics: A;Gene: tolA

2

2

5

Length 248;

9

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A;Reference number: Square of residues 1-84
A;Reference number: Square of residues 1-84
A;Cecession: A$1090; MUID:80156831; PMID:6767609
A;Contents: sequence of residues 1-84
A;Cecession: A$1090
A;Residues: 1-248 <STR>
A;Residues: 1-248 <STR>
A;Ross-references: UNIRROT:P02256
A;Ross-references: UNIRROT:P02256
B;Strickland, W.N.; Strickland, W.N.; Strickland, W.F.; von Holt, C.; Lehmann, A.; Wittmann-Lié
Bur. J. Blochem. 104, 567-578, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus angulations of the sea urchin Parechinus angulation of the sea urchinus ang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tolA protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18] C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cipacession: AG0552
Riparkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connecton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; O'Gaora, P.; Cronin, A.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.S.; O'Gaora, P.; Comin, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A; Stacession: AG0592
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-376 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:AL513382; PIDN:CAD05209.1; PID:g16501979; GSPDB:GN00176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sperm tail-specific protein mst101(2) - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Species: Drosophila hydei
C;Date: 19-711-199 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S51364; S345aan, S.; Buenemann, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KYAKKEKAYAKAKAEAKAAKKA-KAEAKKYAKAAKAEKKEYAA-AEAKYKAEAAKAAAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 122.5; DB 2;
Pred. No. 0.0066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 39.3%; Score 123; DB 1; Best Local Similarity 56.1%; Pred. No. 0.0044; Matches 37; Conservative 7; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKAYAKA---KKAEAKAAK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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Best Local Similarity 51.3
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 KAAKKA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 EAAYEA 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics;
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S51364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Escherichia coli (State 1975)
C;Species: Escherichia coli (State 1975)
C;Species: Escherichia coli (State 1975)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: V00657; Medster, R.E.
J; Bacteriol. 171, 6600-6609, 1989
A;Title: Nucleotide sequences of the tola and tola genes and localization of their produ A;Reference number: Jv0057; MUID: 90078104; PMID: 2687247
A;Accession: Jv0057; MUID: 90078104; PMID: 2687247
A;Accession: Jv0057; MUID: 90078104; PMID: 9148018; PIDN: AAA24683.1; PID: 9148018
A;Residuse: 1-421 < LED:
A;Residuse: 1-421 < L
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HayUNIP
histone H1, gonadal - sea urchin (Parechinus angulosus)
histone H1, gonadal - sea urchin (Parechinus angulosus)
C;Species: Parechinus angulosus (angulate urchin)
C;Date: 31-Mar-1980 #sequence revision 31-Mar-1980 #text_change 09-Jul-2004
C;Date: 31-Mar-1980 #sequence revision 31-Mar-1980 #text_change 09-Jul-2004
C;Accession: A91091, A920586
R;Strickland, W.N.; Strickland, M.; de Groot, P.C.; von Holt, C.; Wittmann-Liebold, B.
Eur. J. Biochem. 104, 559-566, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus ang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-421 <BLAT>
A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960;
A;Experimental source: strain K-12, substrain MG1655
C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t
C;Genetics:
                                                                                                                                 4.
                                                                                                                                                                                                                                                                             48
                                                                                                                                                                                                                        54
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                                                                                                                                                                                                                        1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAA-----KAEKKEYAAAEAKYKAEA
                                                                                                                            6
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                                      Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.9%; Score 131; DB 2; Length 421; 52.6%; Pred. No. 0.0016; ive 9; Mismatches 16; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Start codon: GTG
C;Keywords: nucleotide binding; P-loop; transmembrane protein
P;14-34/Domain: transmembrane #status predicted <MSS>
F;78-301/Domain: helical #status predicted <HSR>
F;78-362/Region: nucleotide-binding motif A (P-loop)
                                                                                                                            Indels
                            Score 132.5; DB 2;
Pred. No. 0.0011;
8; Mismatches 13;
42.3%; Scc. No. v... 58.9%; Pred. No. v... 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tolA protein - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 KKKAEAAEAAAEARKKA 211
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41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| |:|| :|
214 EKAAADKKAAEKA 226
                                                                                                                                                                                                                                                                                                                                                                                                         55 AKAAA-KEAAYEA 66
                                                                                                                        43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                            Local Similarity
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                                      Query Match
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                                                                                 Best Loca
Matches
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3

21; Gaps

Indels

Length 376;

228

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R;Fabry, S.; Mueller, K.; Lindauer, A.; Park, P.B.; Cornelius, T.; Schmitt, R. Curr. Genet. 28, 333-345, 1995
A;Title: The organization structure and regulatory elements of Chlamydomonas histone gene A;Reference number: S59581; MUID:96120862; PMID:8590479
A;Recession: S5988
A;Recession: S5988
A;Recession: S5988
A;Residues: Incleic acid sequence not shown
A;Residues: L-231 cFAB>
A;Cross-references: UNIPROT:Q39576; EMBL:U16726
A;Ross-references: UNIPROT:Q39576; EMBL:U16726
A;Rebry, S.; Ford, C.; Lindauer, A.; Mueller, K.; Cornelius, T.; Schmitt, R.
Submitted to the EMBL Data Library, October 1994
A;Reference number: S62122
A;Reference number: S62122
A;Rocession: S62122
A;Rolecule type: DNA
A;References: EMBL:U16726; NID:g571479; PIDN:AAA98452.1; PID:g571480
C;Genetics: C. 1017.
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A;Status: nucleic acid sequence not shown; translation not shown
A;Nolecule type: DNA
A;Residues: 1-372 <TIGR>
A;Cross-references: UNIPROT:P44678; GB:U32722; GB:L42023; NID:g1573348; PIDN:AAC22041.1;
B;Sen, K.; Sikkema. D.J.; Murphy, T.F.
B;Sen, K.; Sikkema. D.J.; Murphy, T.F.
A;Title: Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA ar
A;Reference number: JC5212; MUD:97080550; PMID:8921895
A;Accession: JC5212
A;Ac
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Outer membrane integrity protein tolA - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

B;Fleischann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Flandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800
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A;Note: the authors translated the codon CGT for residue 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 62/3; 101/3
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%; Score 117.5; DB 2;
46.6%; Pred. No. 0.016;
iive 10; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 37.7%; Score 118; DB 2 Local Similarity 55.6%; Pred. No. 0.01; nes 35; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 46.6%
Matches 34; Conservative
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Best Local S:
Matches 35,
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G64064
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83525
R;Stover, CK.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathona, A;Reference number: A82950; MUID: 20437337; PMID: 10984043
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A;Experimental source: strain PAO1
                                                                  represe
                   Eur. J. Biochem. 225, 1089-1095, 1994
Aftitle: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif 3
1pha-helical rods within the extremely elongated spermatozoa of Drosophila hydei.
A;Reference number: S51364; MUID:95045538; PMID:7957199
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histone H1 - Chlamydomonas reinhardtii
histone H1 - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S59589; S62122
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TolA protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-163,'E',164-236,'Q',237-254,257-320,'E',321-1390 <NEW>
A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
C;Genetics:
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Pred. No. 0.011;
7; Mismatches 22; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                A,Accession: S51364
A,Status: nucleic acid sequence not shown
A,Molecule type: DNA
A,Residues: 1-1390 «NEE>
A,Cross-references: UNIPROT:008696; EMBL:X7346
R,Neesen, J.; Heinlein, U.A.O.; Buenemann, H.
submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: mst101(2)
A;Cross-references: FlyBase:FBgn0011816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.8%;
59.7%;
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Best Local Similarity 51.5%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: S34153
A;Accession: S34154
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Aarkaa 220
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A;Molecule type: DNA
A;Residues: 1-347 <STO>
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C,Genetics:
A,Gene: tolA; PA0971
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Distone H1 (clone TH315) - wheat
Cipacies: Triticum aestivum (common wheat)
Cipacies: Triticum aestivum (common wheat)
Cipacies: Triticum aestivum (common wheat)
Cipacession: To6241
RiTaoka, K.; Ohtsubo, N.; Fujimoto, Y.; Mikami, K.; Meshi, T.; Iwabuchi, M.
Plant Cell Physiol. 39, 294-306, 1998
Plant Cell Physiol. 39, 294-306, 1998
A;Title: The modular structure and function of the wheat H1 promoter with S phase-specifi A;Accession: T06241
A;Accession: T06241
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-284 <TAO>
A;Molecule type: DNA
A;Cross-references: UNIPROT:065794; EMBL:DB7064; NID:g2980890; PIDN:BAA25203.1; PID:g2980
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                                                                           mat101-1 protein - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
S;Species: S;Species: Drosophila hydei
S;Species: Drosophila hydei
S;Species: D;Species: D;
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histone H1-gamma, embryonic - sea urchin (Strongylocentrotus purpuratus)
histone H1-gamma, embryonic - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A26721
R;Knowles, J.A.; Lai, Z.C.; Childs, G.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----KKEYAAAEAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.7%; Score 115; DB 2;
49.4%; Pred. No. 0.024;
tive 4; Mismatches 1
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C;Superfamily: neurofilament triplet H protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 KCAEAAKKEKEAAEKKKCAEA 144
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C;Superfamily: histone H1
C;Keywords: DNA binding; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 49.4#
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 K 212
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Stops 12
St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC013B
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Jul, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-388 «KUR»
A;Cross-references: UNIPROT:Q8ZGZ2; GB:AL590842; PIDN:CAC89966.1; PID:g15979190; GSPDB:C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
AC0138
TolA colicin import membrane protein [imported] - Yersinia pestis (strain C092)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KKYAKKEKAYAKAK-----KAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAK 56
     23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.4%; Score 117; DB 2; Length 388;
49.3%; Pred. No. 0.018;
tive 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KYAKKEKAYAKAKKAEAK---AAKKAKAEAKKYAKAAKAEKKEYAA---
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1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 KKKTAAKKAKKPAAKKA 188
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C, Superfamily: histone H1
C, Keywords: chromosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 YKAEAAKAAAKEAAYEA 66
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228 AEAKAATEAKRKA 240
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Matches 33; Conservative
                                                                                                                                                                                          54 AAKAAAKEAAYEA
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Best Local Similarity
Matches 38; Conservat
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219 KAAADAA 225
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-206 <HIL>
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A; Status: preliminary
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ABIGNOP 15
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C; Species: Listeria innocua
C; Saccesion: AE1669
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
C; Donninguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D; Jonnes, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-243 < GLA>
A; Cross-references: UNIPROT:092A67; GB:AL592022; PIDN:CAC97285.1; PID:gl6414556; GSPDB:C
C; Genetics:
C; Genetics:
C; Genetics:
C; Genetics:
C; Schuetics:
C; Sc
Mol. Cell. Biol. 7, 478-485, 1987

A;Title: Isolation, characterization, and expression of the gene encoding the late histch R;Reference number: A26721; MUD:87172742; PMID:3031476
A;Accession. A26721
A;Accession. A26721
A;Accession. A. Accession. BNA
A;Residues: 1-217
A;NO A;Accession. BNA
A;Residues: 1-217
A;NO A;Accession. BNO A;Accession. Bistone H1
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
F;2-217/Product: histone H1-gamma, embryonic #status predicted AMT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEK----AYAKAKKAEAK-----AAKKAKAEAKKYAKAAK---AEKKEYAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKEKAYAKAKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAE--AKYKAEAAKAA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.9%; Score 112.5; DB 2; Length 217; 49.4%; Pred. No. 0.026; vative 3; Mismatches 21; Indels 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: December 14, 2004, 05:52:13 Job time : 15.1772 secs
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199 KPAKKAAKPAKKAAKPA 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 49.4%
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 KEKAAAEA 177
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 05:47:53 ; Search time 74.076 Seconds

(without alignments)
512.646 Million cell updates/sec

Title: US-10-792-311-4
Perfect score: 313
Sequence: 1 AKKYAKKEKAYAKKAEAK......BAKYKAEAAKAAAKEAAYEA 66

Sequence: 1 AKKYAKKEKAYAKAKKAEAK.. Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: UniProt 02:*

: UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	is escherichia	65 escherichia	34 escherichia			al shigella fl	0						ko yarrowia li	164 yersinia pe		96 drosophila				00 pseudomonas	Q6sg84 uncultured	17978 unculture					bordetell	109 parechinus			39 pseudomonas
Des	Q7agi8	Q8x965	P19934	Q8fjt1	Q7c2q4	083sa1	Q9cm7	Q8zqt6	P02	Q9wwx1	Q88ni6	Q8z8c1	Q6cdx0	Q74w64	Aas	008696	Q937k4	Q6d7£3	Q7rc08	P50600	068	Aar	P44678	Q7n6t7	Q8zgz2	Q8czz8	Q7w477	Q7m409	Q7wfn5	008695	Q87y3
ID	Q7AG18	Q8X965	TOLA ECOLI	Q8FJT1	Q7C2Q4	Q83SA1	Q9CIM70	Q8ZQT6	H1_PARAN	Q9WWX1	Q88N16	Q8Z8C1	Q6CDX0	Q74W64	AAS61283	MST2_DROHY	Q937 <u>K</u> 4	Q6D7F3	Q7RC08	TOLA_PSEAE	Q6SG <u>8</u> 4	AAR37978	TOLA_HAEIN	Q7N6T7	Q82GZ2	Q8CZZ8	Q7W477	Q7M409	Q7WFNS	MST1_DROHY	Q87Y39
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* Query Match	42.3	42.3	41.9	40.9	40.7	40.7	40.4	39.8	39.3	39.1	39.1	39.1	39.0	38.8	38.8	38.8	38.3	38.3	38.3	38.2	37.7	37.7	37.5	37.4	37.4	37.4	37.1	36.9	36.9	36.7	36.7
Score	132.5	132.5	131	128	127.5	127.5	126.5	124.5	123	122.5	122.5	122.5	122	121.5	121.5	121.5	120	120	120	119.5	118	118	117.5	117	117	117	116	115.5	115.5	115	115
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Q7tnl7 mus musculu	O01395 drosophila	O65794 triticum ae	Q8k1s9 mus musculu	P07796 strongyloce	Q92a67 listeria in	Q6miu4 bdellovibri	Cae80819 bdellovib	Q9zhc5 mycobacteri	Q8y5w4 listeria mo	Q6n8x8 rhodopseudo	Cae27215 rhodopseu	P06144 lytechinus	Q84nf9 vicia hirsu
Q7TNL7	MST3 DROHY	065794	Q8K1S9	H1G STRPU	Q92 <u>A</u> 67	Q6MIU4	CAE80819	DBH MYCSM	Q8Y5W4	Ø6N8X8	CAE27215	H1 LYTPI	Q84NF9
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      54
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MEDLINE=90078104; PubMed=2687247;
Levengood S.K., Webster R.E.;
"Nucleotide sequences of the tolA and tolB genes and localization of their products, components of a multistep translocation system in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=KIZ / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
                                                     STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                        42.3%; Score 132.5; DB 2; Length 394; 58.9%; Pred. No. 0.0049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=tolA; Synonyms=cim, excC, lky; OrderedLocusNames=b0739; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   394 AA; 40517 MW; 5B58D8E8230BDE28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bscherichia coli.";
J. Bacteriol. 171:6600-6609(1989)
                                                                                                                                                                                                                                                       EMBL; AE005252; AAG55075.1; -. PIR; F90725; F90725.
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214 EKAAADKKAAEKA 226
                                                                                                                                                                                                                                                                                                                   HSSP; P19934; 1TOL.
InterPro; IPR010528; TolA.
Pfam; PF06519; TolA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 AKAAA-KEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
SEQUENCE 394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
  NCBI_TaxID=83334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=562;
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P19934;
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TOLA ECOLI
TOLA ECOLI
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.;
"Filamentous phage infection: crystal structure of g3p in complex with
"Filamentous phage infection: crystal structure of g3p in complex with
its coreceptor; the C-terminal domain of TolA.";
Structure 7:711-722(1999)
-!- FUNCTION: Involved in the tonB-independent uptake of group A
colicins (colicins A, E1, E2, E3, and K). Necessary for the
colicins to reach their respective targets after initial binding
to the bacteria. Also involved in the translocation of
bacteriophage DNA.
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T., "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tandem repeats of [EDA]-K(1,2)-A(2,4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Derouiche R., Gavioli M., Benedetti H., Prilipov A., Lazdunski C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: Interacts, via domain II, with porins ompC, phoE and
                                                                                                                                                                                                                                                                                                                                                                             Levengood S.K., Beyer W.P. Jr., Webster R.E.;
"TolA: a membrane protein involved in colicin uptake contains an extended helical region.";
Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "TolA central domain interacts with Escherichia coli porins.";
EMBO J. 15:6408-6415(1996).
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DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421
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EMBL; AAC00017, AAC73833.1; -.
EMBL; D90713; BAS405.1; -.
PIK; JV0057; JV0057.
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INTERACTION WITH PORINS.
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EchoBASE; EB1000; -.
EcoGene; EG11007; tolA.
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421
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Query Match
Best Local Similarity
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                                                                                                                                   NCBI_TaxID=623;
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01-JUN-2003
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                                                                                                                                                                                                                   1 AKKYAKKEKAYAKAK-----KAEAKAAKKAKAEAKKYAK-----AAKAEKK-EYAAAEA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEKAYAKAK ----KAEAKAKKAKAKAKA-YAKAAKA----EKKEYAAAEA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-2288234; PubMed=12471157; Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Burland V., Plunkett G. III, Redford P., Hockett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli."; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

EMBL, AR01657; AAN79291.1; -...
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Pred. No. 0.012;
8; Mismatches 17; Indels 12; Gaps
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli 06.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                              16; Indels 12;
                                                                                                                                                                       41.9%; Score 131; DB 1; Length 421; 52.6%; Pred. No. 0.0068; tive 9; Mismatches 16; Indels 1
                                                                                                                                                      43156 MW; 8B2F52B4B97C655E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 AA; 43184 MW; DB296626F056D385 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                  421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=06:H1 / CFT073 / ATCC 700928;
                                                                                                                                                                                                                                                                                                                                                     Created)
 13.
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                                                                                                                                                                                                                                                                             194 KKKAEAAEAAAEARKKA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KYKAEAAKAAAKEAAYEA 66
                                                                                                                                                                                                                                                          49 KYKAEAAKAAAKEAAYEA 66
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Local Similarity 52.6%;
Hes 41; Conservative
                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                   Best Local Similarity 52.6
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Complete proteome.
SEQUENCE 421 AA; 4318
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3351
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                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Zanang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                     STRAIN=2457T;

WEDLINE=22590274; PubMed=12704152;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
Mau B., Perna M.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T.";
Infect. Immun. 71:2775-2786(2003).
EMBL; AR016979; AAP16075.1;
InterPro; IPR010528; TolA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Membrane spanning protein, required for outer membrane integrity.
Name=tolA, OrderedLocusNames=SF0558;
Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacīeria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
NCBI_TaxID=623;
                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.7%; Score 127.5; DB 2; Length 56.7%; Pred. No. 0.013; ive 6; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEAM; PF06519; TolA; 1.
SEQUENCE 413 AA; 42355 MW; 93E10F2C5DE60DE8 CRC64;
Q7C2Q4 PRELIMINARY; FAI, Q7C2Q4; Q7C2Q4; Q7C2Q4; Q7C2Q4; Q7C2Q4; G7EMBLrel. 27, Created) 05-UUL-2004 (TrEMBLrel. 27, Last sequence update) 05-UUL-2004 (TrEMBLrel. 27, Last annotation update) Membrane spanning protein.
Name=tolA; OrderedLocusNames=S0571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      413 AA.
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Pfam; PF06519; TolA; 1.
Complete proteome.
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Parechinus angulosus (Angulate sea urchin).
Bukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euchinoidea, Echinacea, Echinoida, Echinidae, Parechinus.
                                                                               McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The primary structure of histone H1 from sperm of the sea urchin Parechine angulosus. 1. Chemical and enzymatic fragmentation of the protein and the sequence of amino acids in the four N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=80156832; PubMed=7363905;
Strickland W.N., Strickland M., Brandt W.F., von Holt C., Lehmann A.,
Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 39.8%; Score 124.5; DB 2; Length 407; Best Local Similarity 47.8%; Pred. No. 0.022; Matches 43; Conservative 6; Mismatches 10; Indels 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=80156831; PubMed=6767609;
Strickland W.N., Strickland M., de Groot P.C., von Holt C.,
Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 AA; 41865 MW; 2534352116602D75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAYAKA---KKAEAKAAK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 AAAEAKYKAEAA-----KAAAKEAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cyanogen bromide peptides.";
Eur. J. Biochem. 104:559-566(1980).
                             STRAIN=LT2;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                     Nature 413:852-856(2001).
EMBL; AE008730; AAL19691.1;
HSSP; P19934; 1TOL.
                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR010528; TolA. Pfam; PF06519; TolA; 1. Complete proteome.
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  SEQUENCE FROM N.A.
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H1_PARAN
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                                                                                                                                                                     1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKK-EYAAAEAKYKAEAAKAAA
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MEDLINE=21145866; PubMed=11248100;
MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella miltocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE006136; AAK03052.1; -..
HSSP; P01096; IGMJ.
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
101-protein, membrane spanning protein.
Name=tolA, OrderedLocusNames=STM0747;
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Bacteria; Proteobacteria; Salmonella.
NCBI TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
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Pasteurellaceae; Pasteurella.
                                                     Match 40.7%; Score 127.5; DB 2; Length 413; Local Similarity 56.7%; Pred. No. 0.013; es 38; Conservative 6; Mismatches 20; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.4%; Score 126.5; DB 2; Length 389; 52.0%; Pred. No. 0.014; ive 9; Mismatches 12; Indels 15
42355 MW; 93E10F2C5DE60DE8 CRC64;
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Last annotation update)
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InterPro; IPR009528; TolA.
InterPro; IPR000533; Tropomyosin.
Pfam; PP06519; TolA; 1.
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PRINTS; PR00194; TROPOMYOSIN.
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01-JUN-2001 (TrEMBLrel. 17,
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tes 39; Conservative
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                                                                                                                                                                                                                                                                                                                                          197 AEARKKA 203
                                                                                                                                                                                                                                                                                     60 KEAAYEA 66
413 AA;
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SEQUENCE
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DB 2; Length 372;

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1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKA--EAAKAA 58
                      Pfam; PF06519; TolA; 1.
PRINTS; PR06624; HISTONEH5.
TIGRFAM; TIGR01352; tonB Cterm; 1.
SEQUENCE 372 AA; 40133 MW; 87P49785ECC3C0BC CRC64;
                                                                               39.1%; Score 122.5; DB 51.5%; Pred. No. 0.029; ive 10; Mismatches 1
          InterPro; IPR006260; TonB_C.
                                                                                           Local Similarity 51.5
nes 35, Conservative
                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                    205 AEDAKKKA 212
                                                                                                                                                                              59 AKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=160488;
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Q88N16;
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                                                                                                                                                                                GO; GO:0016020; C:membrane; IEA.
GO; GO:0000786; C:nucleosome; IEA.
GO; GO:0000534; C:nucleosome; IEA.
GO; GO:000534; C:nucleus; IEA.
GO; GO:003288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
GO; GO:0003577; F:DNA binding; IEA.
GO; GO:0008565; F:protein transporter activity; IEA.
GO; GO:0005334; P:nucleosome assembly; IEA.
GO; GO:0015031; P:protein transport; IEA.
InterPro; IPR005819; Histone—H5.
InterPro; IPR010528; TolA.
                                                                                                                                                                   3 KYAKKEKAYAKAKKAEAKAAKKA-KAEAKKYAKAKAKAEKKEYAA-AEAKYKAEAAKAAAK 60
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.;
"The Pseudomonas putida peptidoglycan-associated outer membrane
lipoprotein (PAL) is involved in maintenance of the integrity of the
cell envelope.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rodriguez-Herva J.J., Ramos J.;
"Characterization of an OprL null mutant of Pseudomonas putida.";
J. Bacteriol. 178:5836-5840(1996).
                                                                                                                                            .;
7
                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
NCBI_TaxID=303;
Pfam; PP00538; Linker histone; 1.
PRINTS; PR00624; HISTONBHS.
ProDom; PD000373; Linkerhist_N; 1.
SMART; SM00526; H1S; 1.
Chromosomal protein; Direct protein sequencing; DNA-binding;
Multigene family; Nuclear protein; Sperm.
                                                                                                                  39.3%; Score 123; DB 1; Length 248; 56.1%; Pred. No. 0.019; artive 7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=mt-2;
Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, X74218; CAB50780.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ramos-Gonzalez I.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                          248 AA; 26387 MW; 1B25B3F136541947 CRC64;
                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                            Created)
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Bacteriol. 178:1699-1706(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96422022; PubMed=8824639;
Rodriguez-Herva J.J., Ramos J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96198174; PubMed=8626299;
                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                           37; Conservative
                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                      180 KAAKKA 185
                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas putida.
                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                 61 EAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                               Fold protein.
                                                                                            SEQUENCE
                                                                                                                  Query Match
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Q9WWX1
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1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKA--EAAKAA 58
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GO:001086; C:nucleosome; IEA.
GO:000786; C:nucleosome; IEA.
GO:0030288; C:nucleosome search 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-22423060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nartins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nolson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Medler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.
K.Gewitz C., Elsen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Embriton Wicrobiol, 4:799-808(2002). EMBL; AROMG645.1; -. HSSP; P50600; 1LR0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 39.1%; Score 122.5; DB 2; Length Local Similarity 51.5%; Pred. No. 0.029; Length 85; Conservative 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Biopolymer transport protein TolA.
Name=ColA, OrderedLocusNames=PP1221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas putida (strain KT2440)
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InterPro; IPR010528; TolA.
InterPro; IPR006260; TonB_C.
Pfam; PF06519; TolA; 1.
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A Goffard N., Frangeul L., Aigle M., Anthousard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
B Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyee P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozter-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.;
T. "Genome evolution in yeasts.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=91001 / Biovar Mediaevalis; Spang J., Pei D., Wang J., Zhou Song Y., Tong Z., Wang L., Han Y., Zhang J., Chen F., Qin H., Wang J., Li S., Guo Z., Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yersinia pestis.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
ORFNames=YAL10B20570g;
Yarrowia lipolytica (Candida lipolytica).
Bukaryota; Fungi; Ascomycota; Saccharomycottes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.0%; Score 122; DB 2; Length 71
50.7%; Pred. No. 0.056;
tive 8; Mismatches 18; Indels
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
BMB., AE07130; AAS61283.1;
InterPro; IPR010528; TolA.
PFam; PF06519; TolA; 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; CR382128; CAG83395.1; -.
SEQUENCE 713 AA; 77807 MW; 5DD84D2C34CF55AC CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Tola Colicin import membrane protein.
Name=tola, OrderedLocusNames=YP1033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 50.7
Matches 35, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 430:35-44(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 AA;
                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=CLIB99;
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                                                                                                                                                                                                                                        STRAIN=CLIB99;
                                                                                                                                                                                                                                                                         GENOLEVURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  074W64
                    셤
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          148 AKKAAEKQQADIAKKKAEDEAKKKAEEEAK---KAAAEEAKKKAAEDAKKKAAEEAKKKA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Bashaman D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quall M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Mhitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKA---KKAEAKAAK------KAKAEAKKYAKAAKAEKKEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2004 (TrEMBLrel. 28, Created)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp| P38678 Neurospora crassa Glucan synthase-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 AA; 38804 MW; EC21F2C4767A8A42 CRC64;
                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Pred. No. 0.029;
4; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    713 AA.
                                                                                                                                                                                                                                                                                                    376 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=tolA; OrderedLocusNames=STY0793, t2129;
Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 185:2330-2337(2003).
RMBL; ALG67268; CAD05209.1; -.
EMBL; AE016841; AA069743.1; -.
HSSP; P19934; ITOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 AAAEAKYKAEAAKAAAKE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.1%;
51.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR010528; TolA.
Pfam; PF06519; TolA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413:848-852(2001).
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                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                      205 AEDAKKKA 212
                                                                             59 AKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                   Q8Z8C1; Q7C8P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tola protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oecoxo;
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RESULT 12
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10 0828C1
DT 01-MA
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Gaps

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Length 713;

630

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Zhou

DB 2; Length 401;

RESULT 13
Q6CDX0
ID Q6CDX
AC Q6CDX
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C

Matches

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23

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1 AKKYAKK-EKAYAKA-KKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-91001 / Biovar Mediaevalis;
STRAIN-91001 / Biovar Mediaevalis;
SONG W., Tong C., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
Yang R.,
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017130; AAS61283.1; -.
SEQUENCE 401 AA; 41868 MW; 43D682DE91CF1301 CRC64;
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yersinia pestis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
NCBI_TaxID=632;
                                                     3;
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Best Local Similarity 56.9%; Pred. No. 0.037;
Matches 37; Conservative 7; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAR-2004 (TrEMBLrel. 27, Created)
24-MAR-2004 (TrEMBLrel. 27, Last sequence update)
04-MAY-2004 (TrEMBLrel. 27, Last annotation update)
TolA colicin import membrane protein.
TOLA OR YP1033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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234 AADAA 238
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AAS61283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
AAS61283
DA AAS611
AC AAS61
DT 24-MA
DT 24-MA
DT 04-MA
DT 04-MA
DT 04-MA
DT 06-MA
DE TOLA
OC BACTE
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1 AKKYAKK-EKAYAKA-KKAEAKAAKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAA 58

Gaps

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single
  TYPE: amino acid
STRANDEDNESS: single
                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino ErrANDEDNESS: Bing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAKEAA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 64, Application US/08460971A; Patent No. 6150168; Patent No. 6150168; Barbard INFORMATION:
GENERAL INFORMATION:
APPLICANT: Work, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65; CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                  OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-167-641C-64
                                                                                                                                                                                                                                                                                                                                                                       Query Match 39.1%; Score 104; DB 3; Length 100; Best Local Similarity 58.2%; Pred. No. 0.00082; Matches 32; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: 631 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STREET: Suite 4700 CITY: Los Angeles STREET: California COUNTRY: U.S.A.

ZIP: JOHN TYPE: STORED COMPUTER READABLE FORM: MEDIUM TYPE: STORED COMPUTER: STORED COMPUTER: STORED COMPUTER: TBM COMPATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/460,971A FILING DATE: Unne S, 1995 CLASSIFTCATION NUMBER: 07/655,389 FILING DATE: March 20, 1993 APPLICATION NUMBER: 07/655,389 FILING DATE: March 20, 1993 APPLICATION NUMBER: PCT/US93/02725 FILING DATE: March 19, 1993 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 489-1600
TELERX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTER.57ICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-460-971A-64
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1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAKEAA 53
                                                                                                                                                                                                                                                                    Sequence 64, Application US/08462040

| Sequence 64, Application US/08462040
| Patent No. 6177554
| Cantenan No. 6177554
| APPLICANT Woo, Savio L.C.
| APPLICANT Smith, Louis C.
| APPLICANT Smith, Louis C.
| APPLICANT Gottchalk, Stephen TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 65
| CORRESPONDENCE ADDRESS: ADORESSE: Lyon & Lyon STREET: Suite 4700
| STREET: Suite 4700
| CITY: Los Angeles STRATE: California COUNTRY: U.S.A.
| COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear _
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be
OTHER INFORMATION: present or absent.
OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be CTHER INFORMATION: present or absent.

US-08-460-971A-64
                                                                                                             Query Match 39.1%; Score 104; DB 3; Length 100; Best Local Similarity 58.2%; Pred. No. 0.00082; Matches 32; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BACRAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
OCHWARE FASTEM: IBM P.C. DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: Docember 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: 07/855,389
FILING DATE: March 10, 1993
APPLICATION NUMBER: 20, 1993
APPLICATION NUMBER: 20, 1993
APPLICATION NUMBER: 212/078
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32, 120/078
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 212/078
TELECOMMUNICATION NUMBER: 212/078
TELECOMMUNICATION NUMBER: 212/078
TELECOMMUNICATION NUMBER: 32, 1800
TELERAX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TTYPE: amino acids
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US-08-462-040-64

2; Gaps Query Match
Best Local Similarity 58.2%; Pred. No. 0.00082;
Matches 32; Conservative 4; Mismatches 17; Indels

2;

Search completed: December 14, 2004, 05:50:17 Job time: 16.8559 sec8

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Sequence 64, Application US/08167641C

Patent No. 6033884

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: WETHODS OF USE
NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Smite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FERSEEG FOR Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                             TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 maino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,3
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-167-641C-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
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Patent No. 5994109

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Grith, Louis C.
APPLICANT: Grith, Louis C.
APPLICANT: Grith, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: MCTHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.1%; Score 104; DB 3; Length 56; 58.2%; Pred. No. 0.00046; tive 4; Mismatches 17; Indels
                                                                                                                  CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997

PRIOR APPLICATION: 514

PRIOR APPLICATION NUMBER: US 60/032,436

ATFORNEY/AGENT INPORMATION:

NAME: S111/van, Sally A.

REGISTRATION NUMBER: 32,064

REGISTRATION NUMBER: 32,064

REGISTRATION NUMBER: 33-95

TELEFPHONE: 303-499-8089

TELEFPHONE: 303-499-8089

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LEMOTH: 56 amino acids

TVODE: Amino acids

TVODE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRESENG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: June 5, 1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSS: not relevant not relevant
                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.2'
...hes 32; Conservative
                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: N
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
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US-08-460-890A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
COUNTRY:
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1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAKEAA
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US-08-460-890A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 100,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 39.1%; Score 104; DB 2; Length 10 Best Local Similarity 58.2%; Pred. No. 0.00082; Matches 32; Conservative 4; Mismatches 17; Indels
            APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/066
TELECOMMUNICATION INFORMATION:
December 14, 1993
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEKA----AKKAYKK-------EAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYNTHETIC
                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION UNBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
SOFTWARE: PATENTIN Ver. 2.1
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                  Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                                                                                                           Query Match 40.8%; Score 108.5; DB 4; Best Local Similarity 55.7%; Pred. No. 0.0014; Matches 34; Conservative 7; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-AAEAKKKAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.3%; Score 104.5; DB 4 51.8%; Pred. No. 0.00025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liotta, Dennis C.
APPLICANT: Petros, John A.
APPLICANT: Wey, Shlow-Jyi
APPLICANT: Karr, Joan F.
APPLICANT: Karr, Joan F.
TITLE OF INVENTION: Polycationic Oligomers
WUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Greenlee, Winner and Sullivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13565
LENGTH: 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09405743A Patent No. 6514938 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08993008A
Patent No. 6153596
                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.3
Best Local Similarity 51.8
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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US-09-405-743A-1
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US-08-993-008A-6
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                                                           APPLICANT: NO. 0/1/13/
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
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US-09-248-796A-26122

US-09-248-796A-26122

US-09-248-796A-26122

Sequence 26122, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: USCALL 1999-02-12

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 26122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (42)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknd
US-09-248-796A-26122
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 KKBEBAKKKBEBAKKKABEBAKKKABBAKKVBBAKKABBAKKABBBARKKA 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 110.5; DB 4; Length 148; Pred. No. 0.00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 110; DB 4; Length 264;
Pred. No. 0.00056;
4; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                      Sequence 26989, Application US/09248796A Patent No. 6747137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Candida albicans US-09-248-796A-26989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Conservative
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Matches 30; Conserv
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Best Local Similarity
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US-09-489-039A-13565
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                     -09-248-796A-26989
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Query Match
Best Local Similarity 45.9
Matches 50; Conservative
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                                                                                                61 EAAYEA 66
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US-09-405-743A-2
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LENGTH: 45
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2
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                                          Gaps
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                                        21;
                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09405743A

Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeada Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REPREBNCE: 60807-A
GURRENT APPLICATION NUMBER: US/09/405,743A
GURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 6
LENGTH: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 87.6%; Score 233; DB 4; Length 86; Best Local Similarity 62.8%; Pred. No. 9.2e-17; Matches 54; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.4%; Score 198; DB 4; Length 66; 80.3%; Pred. No. 2.2e-13; ive 2; Mismatches 1; Indels
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: PEPTIDE
US-09-405-743A-6
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DB 4;
Query Match 92.3%; Score 245.5; DB 4; Best Local Similarity 72.7%; Pred. No. 4.6e-18; Matches 56; Conservative 0; Mismatches 0;
                                                                               1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK-
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                                                                                                                                                                                     61 YKAEAAKAAAKEAAYEA 77
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ORGANISM: Artificial Sequence
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Matches 53; Conserv
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US-09-405-743A-6
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LENGTH: 66
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                           .---- 39
1 AKKYAKKEKAY--AKKAE-KAAK--KAEAKAY-KAAEAKKK----AEAKYKAEAAKAAAK 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09405743A
PREEL NO. 6514338
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TILLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT BLING DATE: 199-09-24
NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                        APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
TITLE REPERBLOE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 45;
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OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: PEPTIDE

US-09-405-743A-7
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Pred. No. 3.3e-07;
0; Mismatches 5;
                                                                                                                                                                                                                                                     Sequence 7, Application US/09405743A Patent No. 6514938 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 68.4%;
Matches 39; Conservative
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Sequence 16, Appl Sequence 10, Appl Sequence 10, Appl Sequence 2, Appli Sequence 2, Appli Sequence 13743, A Sequence 6321, Ap

Sequence 41, Appl Sequence 39148, A

2, Appli 2, Appli 5734, Ap 8, Appli 8, Appli 16, Appl

Sequence Sequence Sequence

Sequence 16, P. Sequence 10, P.

US-08-293-284A-2 US-08-898-300-2 US-09-543-681A-5734 US-09-115-746-8 US-08-346-894-16 US-08-346-894-16 US-08-293-284A-16 US-08-216-894-10 US-09-115-746-10 US-09-115-746-10 US-09-115-746-10 US-09-115-746-10 US-09-115-746-10 US-09-115-746-10 US-09-115-746-2 US-09-115-746-10 US-09-115-746-10 US-09-328-352-6321 US-09-328-352-6321 US-09-2770-767-39148

Sequence:

Run on:

Searched:

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Sequence 2, Appli
Sequence 26989, A
Sequence 26122, A
Sequence 13565, A
Sequence 6, Appli
Sequence 64, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 201, Appl
Sequence 29981, Appl
Sequence 29881, Appl
Sequence 29881, Appl
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                                                                                                        December 14, 2004, 05:47:53; Search time 15.7131 Seconds (without alignments) 236.351 Million cell updates/sec
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Sequence 7,
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/ReZOMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-405-743A-3

US-09-405-743A-5

US-09-405-743A-6

US-09-405-743A-6

US-09-405-743A-7

US-09-405-743A-2

US-09-405-743A-2

US-09-405-743A-2

US-09-405-743A-1

US-09-489-039A-13565

US-09-489-039A-13565

US-09-93-008A-6

US-08-460-971A-64

US-08-460-971A-64

US-08-460-971A-64

US-08-460-971A-64

US-08-460-971A-64

US-09-91A-291A-291A

US-09-205-491A-29581

US-09-213-25-5169

US-09-328-32A-504

US-09-328-32A-504

US-09-328-32A-504

US-09-328-32A-504

US-09-32B-32B-5

US-09-32B-32B-5

US-09-248-796A-18922

US-09-248-796A-18922
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                                                                                                                                                                                                                                                                                                                    478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyright
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                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180.5
134.5
110.5
110
108.5
104.5
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Database

Result

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Sequence 3, Application US/09405743A; Sequence 3, Application US/09405743A; Patent No. 651493B; GAREAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd., TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS; FILE REFERENCE: 60807-A (60807-A); CURRENT APPLICATION NUMBER: US/09/405,743A; NUMBER OF SEQ ID NOS: 7; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 3; LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKEKAYAKKAEKAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA
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APPLICANT: Yeda Research and Development Co., Ltd.

APPLICANT: Yeda Research and Development Co., Ltd.

TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 5
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 100.0%; Score 266; DB 4; Length 56; Local Similarity 100.0%; Pred. No. 3e-20; nes 56; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description of Artificial Sequence: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Description of Artificial Sequence:
) OTHER INFORMATION: PEPTIDE
US-09-405-743A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-405-743A-5; Sequence 5, Application US/09405743A; Patent No. 6514938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DESCRIPTION
US-09-405-743A-5
                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
  US-09-405-743A-3
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Best Local S:
Matches 56
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5, Appli 18922, A 25676, A 27, Appl 27, Appl

Sequence Sequence Sequence

Sequence

5169, Ap 5094, Ap

Sequence

Sequence

100 100 99.5 98

103 103 102.5 101

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7; Gaps
; PRIOR FILING DATE: 2001-02-16; Remaining Prior Application data removed - See File Wrapper or PALM.; NUMBER OF SEQ ID NOS: 78614; SEQ ID NO 59321; SEQ ID NO 59321 I TYPE: PRT TYPE: PRT ORGANISM: Klebsiella pneumoniae

', ORGANISM: Klebsiella pneumoniae
', ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                   Query Match 40.8%; Score 108.5; DB 15; Length 323; Best Local Similarity 55.7%; Pred. No. 0.01; Matches 34; Conservative 7; Mismatches 13; Indels 7;
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Search completed: December 14, 2004, 06:59:41 Job time : 139.937 secs

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FILING DATE: 2000-09-09
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ORGANISM: Salmonella typhi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-282-122A-75772
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-29
PRIOR PLING DATE: 2000-05-29
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/200,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1 SEQ ID NO 55748
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US-10-282-122A-75772

i Sequence 75772, Application US/10282122A

i Publication No. US20040029129A1

i GENERAL INFORMATION:
APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Alaone, Cheryl

APPLICANT: Alaone, Cheryl

APPLICANT: Alaone, Cheryl

APPLICANT: Alaone, Cheryl

APPLICANT: Wall, Daniel

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yearick, John

APPLICANT: Yearick, John

APPLICANT: Forsyth, R.
CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-05-23

PRIOR PPLING DATE: 2000-05-23

PRIOR PPLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-09-66

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-123

PRIOR PLING DATE: 2000-123

PRIOR PLING DATE: 2000-123

PRIOR PLING DATE: 2000-12-2

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ 1D NOS: 78614 SOFTWARE: PatentIn version 3.1 SEQ 1D NO 72645
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42.3%; Score 112.5; DB:
Best Local Similarity 53.5%; Pred. No. 0.0052;
Matches 38; Conservative 5; Mismatches 1.
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Amadio, Carlos
APPLICANT: Haselbeck, Robert
                                                                 CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-02-09
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NAME/KEY: MISC FEATURE
LOCATION: (303)...(303)
OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (78)..(78)
OTHER INFORMATION: X=any amino acid
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ORGANISM: Salmonella paratyphi
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Syskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/202,122A
CURRENT PILING DATE: 2000-03-02-03
PRIOR PELICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,335
PRIOR PELICATION NUMBER: 60/2030,347
PRIOR PELICATION NUMBER: 60/2030,348
PRIOR PELICATION NUMBER: 60/2030,348
PRIOR PELICATION NUMBER: 60/2030,308
PRIOR PELICATION NUMBER: 60/2030,308
PRIOR PELICATION NUMBER: 60/2040,308
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Gaps
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NUMBER OF SEQ ID NOS: 78614
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49.3%; Pred. No. 0.0044;
tive 10; Mismatches 9; Indels 19;
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Mangui, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Carlos
APPLICANT: Application (Applicant)
APPLICANT: Carlos
APPLICANT: Carlos
APPLICANT: Carlos
APPLICANT: Application (Applicant)
APPLICANT: Carlos
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||||| |:| ||
183 AKAAADAKKKAEAEA 197
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
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Haselbeck, Robert
                                  Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                           Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Conservative
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Trawick, Joh
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Best Local Similarity
Matches 37; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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Sequence 75047, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                        Sequence 60543, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin version 3.1
SEQ ID NO 60543
LENGTH: 239
                                                                                                                                                                                                                                                                                                                                                                                                                                Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
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Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robe
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Trawick, John
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Matches 31; Conserv
                                                                                               208 RKKA 211
                                      53 AYEA 56
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US-10-282-122A-75047
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/200,321
PRIOR APPLICATION NUMBER: 60/200,335
PRIOR APPLICATION NUMBER: 60/200,335
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-01-23
PRIOR APPLICATION NUMBER: 60/250,347
PRIOR APPLICATION NUMBER: 60/250,347
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/250,331
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-03-06
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                                                                                                                                                                                                                                                                                                                                       10; Indels 14; Gaps
                                                                                                                                                                                                                     Query Match

44.0%; Score 117; DB 15; Length 389;
Best Local Similarity 55.9%; Pred. No. 0.002;
Matches 33; Conservative 7; Mismatches 15; Indels
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Pred. No. 0.0021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 56483, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                               ORGANISM: Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.0%;
54.7%;
SOFTWARE: Patentin version 3.1
SEQ ID NO 67145
LENGTH: 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Mallone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Wall, Daniel
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US-10-282-122A-56483
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Best Local Similarity
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US-10-282-122A-56483
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THILE MERERANCE: BLITTAN JUNGBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
FRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/200, 848
PRIOR PILING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING NUMBER: 60/253,625
PRIOR PELLING NUMBER: 60/253,625
PRIOR PELLING DATE: 2000-11-22
PRIOR PELLING DATE: 2000-11-22
PRIOR PELLING DATE: 2000-11-22
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-06
TITUE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
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APPLICAMY: Xu, H.,

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-22
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PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2001-02-09
                       PRIOR FILING DATE: 2000-09-09
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-27
PRIOR PILING DATE: 2000-12-29
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 44.0%; Score 117; DB 15; Length 372; Local Similarity 66.0%; Pred. No. 0.0019; nes 31; Conservative 2; Mismatches 12; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAA 53
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Publication No. US20040029129A1
   APPLICATION NUMBER: 60/230,347
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Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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ORGANISM: Pseudomonas putida
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Matches
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APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

APPLICANT: Lis, Doris

TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

CURRENT APPLICATION NUMBER: 45/09/816,989A

CURRENT FILING DATE: 2001-03-23

PRIOR FILING DATE: 1998-09-25 PCT/US99/22402

PRIOR FILING DATE: 1999-09-24

NUMBER: POST OF SEQ ID NOS: 7

SOFTWARE: PATCHTION OF SEQ ID NOS: 7
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APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Ku, H.
TITLE ON INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PAPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PLICATION NUMBER: 60/206,848
PRIOR PLILING DATE: 2000-05-24
PRIOR PLILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/206,335
PRIOR FILING DATE: 2000-05-06
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AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKAEAK--
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Mandy, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Obleen, Kari
APPLICANT: Obleen, Kari
APPLICANT: Obleen, Kari
APPLICANT: Obleen, Wari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09816989A
Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Lis, Dotis
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPRENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENTIN VEYSION 3.1
SEQ ID NO 7
LENGTH: 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 74.4%; Score 198; DB 9; Length 66;
Best Local Similarity 80.3%; Pred. No. 6.2e-12;
Matches 53; Conservative 2; Mismatches 1; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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; Sequence 7, Application US/09816989A, patent No. US20020115103A1; GENERAL INFORMATION: APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 EAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EAAYEA 66
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US-09-816-989A-7
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                                                                                                          APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
PRIOR APPLICATION NUMBER: 2001-03-23
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-25
RIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 00/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR PILING DATE: 1998-09-25
RIOR APPLICATION NUMBER: PCT/US99/22402
RIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---AEAK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 92.3%; Score 245.5; DB 9; Length 77; Best Local Similarity 72.7%; Pred. No. 2.2e-16; Matches 56; Conservative 0; Mismatches 0; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

87.6%; Score 233; DB 9; Length 86;
Best Local Similarity 62.8%; Pred. No. 3.8e-15;
Matches 54; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 6, Application US/09816989A; Patent No. US20020115103A1; GENERAL INFORMATION:
                     Sequence 5, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 YKAEAAKAAAKEAAYEA 56
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
                                                                                            APPLICANT: Gad, Alexander
                                                                    GENERAL INFORMATION:
    US-09-816-989A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-816-989A-6
                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 5
LENGTH: 77
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LENGTH: 86
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Sequence 3, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 2, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 68109,
                                                                                                            December 14, 2004, 05:52:22 ; Search time 138.937 Seconds (without alignments) 143.965 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            '(gnz_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*
'(gnz_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*
'(gnz_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
'(gnz_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
'(gnz_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
'(gnz_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
'(gnz_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
'(gnz_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
'(gnz_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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'(gnz_6/ptodata/1/pubpaa/US010_PUBCOMB.pep:*
'(gnz_6/ptodata/1/pubpaa/US010_NEW_PUB.pep:*
'(gnz_6/ptodata/1/pubpaa/US010_NEW_PUB.pep:*
'(gnz_6/ptodata/1/pubpaa/US010_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                          1585576
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-816-989A-5
US-09-816-989A-5
US-09-816-989A-6
US-09-816-989A-7
US-09-816-989A-7
US-09-816-989A-7
US-09-816-989A-7
US-09-816-989A-7
US-09-816-989A-7
US-10-282-122A-6145
US-10-282-122A-6745
US-10-282-122A-7545
US-10-282-122A-75645
US-10-282-122A-75645
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                1585576 segs, 357178320 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:
                                                                          protein search, using sw model
                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0
seq length: 200000000
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Match Length DB
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43.8
42.7
42.3
41.7
                                                                                                                                                                                                               score:
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245.5
233
198
180.5
134.5
117
117
116.5
113.5
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Maximum DB &
                                                                          OM protein
                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                           Title:
Perfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
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Sequence 3, Application US/09816989A
; Sequence 3, Application US/09816989A
; Patent No. US20020115103A1
; GENERAL INFORMATION:
    THOROMATION:
    APPLICANT: Lis, Doris
    TITLE OF INVENTION:
    TORRENT PAPPLICATION NUMBER: US/09/816,989A
; CURRENT PILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR PILING DATE: 1999-09-25
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 56
                     Sequence 16, Appli
Sequence 201, Appli
Sequence 52, Appl
Sequence 120, App
Sequence 66237, App
Sequence 66337, App
Sequence 9889, App
Sequence 9962, Appli
Sequence 10710, Appli
                                                                                               Sequence 5, Appli
Sequence 11, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 64817, A
Sequence 68769, A
Sequence 68769, A
Sequence 198261,
Sequence 198261,
Sequence 198261,
Sequence 198261,
Sequence 69, Appl
         Sequence
                                                                                                                                                                                                                                      Sequence
US-10-177-725-19
US-10-177-725-69
                                                                                                                                                                                                                            US-10-393-449-19
US-10-393-449-69
                                                                                                                                                                                                                                                           ALIGNMENTS
 US-09-816-989A-3
                                                                                                                                                                                                             92.5
92.5
92.5
110.5
108.5
105.5
104.5
103
102.5
102.5
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101
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96.5
96.5
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94.5
94.5
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RESULT

8 6

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-3

ORGANISM: Artificial Sequence

TYPE: PRI

Query Match 100.0%; Score 266; DB 9; Length 56; Best Local Similarity 100.0%; Pred. No. 1.8e-18; Matches 56; Conservative 0; Mismatches 0; Indels

Search completed: December 14, 2004, 06:01:12 Job time : 62.9072 secs

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To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subcloned from pRBV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-cocurs between the Protein A and rCOP-1 sequences. A methionine residue cocurs between the Protein A and rCOP-1 sequences. A methionine residue from the fusion protein. rCOP-1 sequences. A methionine residue from the fusion protein. rCOP-1-19 contains oligonucleotide duplexes incoding the following segments: YKK, AAE, KAA, KKA, YEA, AKA KEA, incoding the following residue is left behind following CNBr cleavage of the fusion protein. The product prevents or arrests experimental autcoimmune encephalomyelitis. They are used to prevent. The rest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diete deficient in certain conference.
                Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAYAKKAEKAAKKAE------AKAYKAAEAKKKAEAKYKAEAAKA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acids. See also AAQ05664. (Updated on 25-MAR-2003 to correct PA field.)
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47.8%; Pred. No. 0.0006;
tive 6; Mismatches 16; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #13351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU27824 standard; protein; 428 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 12; 25pp; English.
                                                                                                                                                                                                                 89US-00312541.
                                                                                                                                                                               90EP-00301700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 47.8
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 AAK-EAAYE 55
                                                                                                                                                                                                                                                                   (REPK ) REPLIGEN CORP.
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                                                                                                                                                                                                                                                                                                                                            WPI; 1990-255848/34.
                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ06446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 106 AA;
                                                                                                                                                                                                                                    07-FEB-1990;
                                                                                                                                                                                                                 17-FEB-1989;
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                                                                                                                                            22-AUG-1990
                                                                                                        EP383620-A
                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                         Cook KS;
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14; Gaps

Enterobacter cloacae

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3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at firewipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYA--KKEKAYAKKAEKAA----KKAEAKAYK--AAEAKKKAEAKYKAEAAKAAAKEA
                                                                                                                                          Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Gaps
                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.7%; Score 111; DB 6; Length 428; 53.1%; Pred. No. 0.0026; ive 11; Mismatches 11; Indels
                                                                                                                                           Ohlsen KL,
Forsyth RA,
                                                                                                                                          Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 55748; 1766pp; English.
                                                                                                                                           Malone C,
Carr GJ,
                                                                        06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                             21-MAR-2002; 2002WO-US009107.
                                                                                                     2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 53.1%
nes 34; Conservative
                                                                                                                        (ELIT-) ELITRA PHARM INC.
                                                                                                                                           Zamudio C,
Trawick JD,
                                                                                                                                                                      WPI; 2003-029926/02
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                                                                                                                                                                                 N-PSDB; ACA31694.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 428 AA;
        WO200277183-A2
                                                                                                      06-MAR-2002;
                                                               21-MAR-2001;
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                                                                                                                                           Wang L,
Wall D,
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Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD,

2003-029926/02

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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 72645; 1766pp; English.
       06-MAR-2002; 2002US-0362699P.
                                                 (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                 N-PSDB; ACA48591
                                                                                           Wang L,
Wall D,
    the foll anticense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a prointeration of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding colliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of a gene in an operon required for che gene product or that has an activity against a biological pathway required for proliferation for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product is open equired for cellular proliferation of an organism acts; (9) manufacturing an antibiocic; (10) profiling a compound sectivity; (11) aculture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or organism acts; (9) manufacturing an antibiocic; (10) profiling a compound sectivity; (11) a culture compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for the which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for derugived for proliferation in cells other than S, aureus, S, typhimurium, CC for cellular proliferation in cells other than S, aureus, S, typhimurium, a part of the printed specification, but was obtained to patent did not form part of the printed specification, but was obtained to make the propersor of the printed specification, but was obtained to make the 
                                              invention relates to an isolated nucleic acid comprising any one of
Claim 25; SEQ ID NO 75047; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
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%XCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

44 1 AKKYAKKEKAYAKKAEKAA----KKAEAKAYK-AAEAKKKAEA-----KYKAEA 42.7%; Score 113.5; DB 6; Length 407; 49.3%; Pred. No. 0.0014; ive 10; Mismatches 9; Indels 19; Gaps 183 AKAAADAKKKAEAEA 197 45 AKAAA---KEAAYEA 56 37; Conservative Best Local Similarity Query Match g 8 ò

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Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                        Protein encoded by Prokaryotic essential gene #30248.
              ABU44721 standard; protein; 387 AA.
                                          (first entry)
                                                                                    Salmonella paratyphi
                                                                                                  WO200277183-A2
                                          19-JUN-2003
                             ABU44721;
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K. pneumoniae or P. aeruginosa. The present sequence is encoded to the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                 48
                                                                                                                                                                                                     17; Gaps
                                                                                                                                                                  Length 387;
                                                                                                                                                                                                       Indels
                                                                                                                                                                DB 6;
                                                                                                                                                                                                                                            1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-AAEAKKKAEA
                                                                                                                                                                Score 112.5; DB 6
Pred. No. 0.0016;
5; Mismatches 11
                                                                                  tp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                42.3%;
                                                                                                                                                        Query Match
Best Local Similarity 53.5
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                199 ÁEAKKKÁEAÉÁ 209
                                                                                                                                                                                                                                                                                                                           49 A---KEAAYEA 56
                                                                                                                           Sequence 387 AA;
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Recombinant copolymer 1-19, myelin basic protein analogue.
                                            (first entry)
                                 (revised)
                                  25-MAR-2003
                                           03-JAN-1991
                AAR06446;
8X2X55X8
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2001US-00948993. 2001US-0342923P. 2002US-00072851.

06-SEP-2001; 25-OCT-2001; 08-FEB-2002;

21-MAR-2001; 2001US-00815242. 21-MAR-2002; 2002WO-US009107

03-OCT-2002

AAR06446 standard; protein; 106 AA.

RESULT 14 AAR06446

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expressed from the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and woachines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
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Sequence 239 AA;

ï Gaps 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAE-AKYKAEAAKAAAKEAAYE 55 1; DB 5; Length 239; Indels 15; f match 43.8%; Score 116.5; DB 5 Local Similarity 55.4%; Pred. No. 0.00039; les 31; Conservative 9; Mismatchen 1 Query Match Matches 셤

ABU32619 standard; protein; 239 (first entry) Listeria monocytogenes. WO200277183-A2 19-JUN-2003 ABU32619; RESULT 11 ABU32619 THE STATE OF THE S

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Protein encoded by Prokaryotic essential gene #18146.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

03-OCT-2002

21-MAR-2002; 2002WO-US009107

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-0CT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-0072881. 06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, ŭ, Wang

2003-029926/02 WPI; 2003-029926/ N-PSDB; ACA36489 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 60543; 1766pp; English.

the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding The invention relates to an isolated nucleic acid comprising any one of

the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway or the proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound a activity; (11) a culture comprising strains in which the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling a compound a activity; (11) a culture comprising strains in which the extent or which each of the strains is present in a culture or collection of product is overexpressed or underexpressed; (12) determining the extent conversion of an organism. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids required for cellular proliferation in cells or homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, CC fung discovery programs, or for screening homologous nucleic acids caids required for proliferation in cells other than S. aureus, S. typhimurium, CC the target prockaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at 1; 1; Gaps 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAE-AKYKAEAAKAAAKEAAYE 55 DB 6; Length 239; Indels 43.8%; Score 116.5; DB 6; 55.4%; Pred. No. 0.00039; ive 9; Mismatches 15; Best Local Similarity 55.4 Matches 31; Conservative Sequence 239 AA; Query Match ð

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ABU47123 standard; protein; 407 AA RESULT 12 ABU47123

19-JUN-2003 (first entry)

Protein encoded by Prokaryotic essential gene #32650.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Salmomella typhimurium

WO200277183-A2

03-OCT-2002.

21-MAR-2002; 2002WO-US009107

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P

ELIT-) ELITRA PHARM INC.

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, ůů, Wang Wall

2003-029926/02

N-PSDB; ACAS0993

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

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246 26

Gaps

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide for its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding capable of specification or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, (7) identifying a compound that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to the which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                        1 AKKYAKKEKAYAK---KAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                     4
                                                                  Score 117; DB 6; Length 389;
Pred. No. 0.00058;
                                                                                                                              15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #14086.
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Yamamoto R,
                                                                                               Pred. No. 0.00
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU28559 standard; protein; 421 AA
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2002; 2002WO-US009107
                                                                      44.08;
                                                                                               Best Local Similarity 55.9%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Trawick JD,
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Sequence 389 AA;
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                                                                  Query Match
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Wall D,
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ABU28559

ABU28559

ABU2

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screening

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drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at from the properties of the printed specification, but was obtained ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein
                                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides.
  proliferation of an organism. The antisense nucleic acids are useful for
                    identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cossart P;
                                                                                                                                                                                                                                                                                                                                     7 KEKAYAKKAEKAAKKAEAKAYK-----AAEAKKKAEA----KYKAEAAKAAAKEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                         Length 421;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                    44.0%; Score 117; DB 6;
54.7%; Pred. No. 0.00062;
ive 5; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listeria monocytogenes protein #1827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB49123 standard; protein; 239 AA.
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                                                                                                                                                                                                                                                                       Best Local Similarity 54.7
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 RKKA 211
                                                                                                                                                                                                                                                                                                                                                                                                                 53 AYEA 56
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                                                                                                                                                                                                                 Sequence 421 AA;
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                                                                                                                                                                                                                                                           Query Match
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Protein encoded by Prokaryotic essential gene #25712.

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the invention fraintes to an instance and compitating any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated of polypeptide of its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular contiferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation, (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation and that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of the strains is present in a culture or collection of compound activity; (11) a culture comprising strains in which the extent or or which each of the strains is present in a culture or collection of confidentifying proteins or screening for homologous nucleic acids required for proliferation of an organism. The antisense nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, contained for proliferation in cells other than S. aureus, S. typhimurium, contained to the printed specification, but was obtained to the print of the printed specification, but was obtained to the print of the printed specification, but was obtained to the properation of the printed specification, but was obtained to the properation of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 68109; 1766pp; English.
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Carr GJ,
                                                                                                                                                                                                                                                                           21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-GCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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Trawick JD,
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N-PSDB; ACA44055.
                                                                                           Pseudomonas putida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang
Wall
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ï
                     Gaps
                     5
Length 372;
                     12; Indels
Score 117; DB 6;
Pred. No. 0.00055;
                   2; Mismatches
44.0%;
66.0%;
                    31; Conservative
Query Match
Best Local Similarity
                     Matches
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113 REAAEAKKAEDAAKAAEAA--KAAEAKKAAEAKKADEAKKAAEKQQA 157

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7 KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAA

23

Antisense; prokaryotic essential gene; cell proliferation; drug design. Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Protein encoded by Prokaryotic essential gene #24748. Haselbeck R, Yamamoto R, ABU39221 standard; protein; 389 AA Malone C, Carr GJ, 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 21-MAR-2002; 2002WO-US009107. 21-MAR-2001; 2001US-00815242. 06-MAR-2002; 2002US-0362699P. 08-FEB-2002; 2002US-00072851 (first entry) (ELIT-) ELITRA PHARM INC. Pasteurella multocida Zamudio C, Trawick JD, WPI; 2003-029926/02 N-PSDB; ACA43091. WO200277183-A2. 19-JUN-2003 03-OCT-2002. ABU39221; Wang L, Wall D, RESULT 8 ABU39221

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

or screening New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 67145; 1766pp; English.

the nucleic acid inhibits proliferation of a cell. Also included are:

the foll antieense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

the comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell contaming the vector; (3) an isolated continued by the antisense contest acid; (4) an antibody capable of specifically binding cantisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular continued for proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway or that has an activity against a biological pathway or the proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a culture comprising strains in which the est compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a culture comprising strains in which the est compound that inhibits the extent or organism; or (13) identifying the target of a compound that inhibits the contest of compounds activity; (11) a culture compounds activity; (12) determining the extent or product is overexpressed or underexpressed; (12) determining the extent or to which each of the strains is present in a culture or collection of proliferation of an organism. The antisense mucleic acids are useful for dentifying proteins or screening for homologous nucleic acids are useful for each of its organism. The antisense andidate model or activity activity in the province condition or an organism. The antisense andidate model or activity of the strains is drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, R. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at The invention relates to an isolated nucleic acid comprising any tp.wipo.int/pub/published_pct_sequences osteopathic; immunosuppressive; antithyroid; antiinflammatory;

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                                                                                                                                                                                                                                                                                                                                    AAY AAV82571 to AAV82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides (1) for determining the molecular weight invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer accetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, crontact cophoritis, autoimmune haroimmune haemolytic anaemia, autoimmune cophoritis, autoimmune throndomytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic mysocedema, myashhania gravis, contact sensitivity disease, which can be treated include host-versus-graft disease, chronic immune thrombocytopaenia purpura, colitis, contact mediated diseases which can be treated include host-versus-graft disease, colypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer accetate molecules, which makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKABKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAKAEAKKYAKEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective;
                                                                                                                                                                                                                                                                 Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----YKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.9%; Score 180.5; DB 3; Length 109; 45.9%; Pred. No. 5.8e-11; ive 3; Mismatches 3; Indels 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKAEAK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY82572 standard; peptide; 45 AA.
                                                                                                                                                                                                                                                                                                              Claim 10; Page 14; 72pp; English
                                                                                                                                                            (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                                                                               98US-0101693P.
                                                                                                    99WO-US022402.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50; Conservative
                                                                                                                                                                                                                                     WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 ----
                                         WO200018794-A1.
                                                                                                                                                                                                        Gad A, Lis D;
             Unidentified.
                                                                                                                               25-SEP-1998;
                                                                                                 24-SEP-1999;
                                                                       36-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY82572;
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AAY82572
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AC AAX8
DT 28-J
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (2), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune hapenolytic anaemia, autoimmune cophoritis, autoimmune thyroididits, autoimmune uveorefinitis, contact sensitivity disease, chromic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated, mediated diseases which can be treated include host versus-graft disease, and delayed-type hypersensitivity. The
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antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitute; graves disease; Gulliain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0101693P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (YEDA ) YEDA RES & DEV
(TEVA-) TEVA PHARM USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-317499/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                 WO200018794-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-1998;
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Matches
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which to marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified modecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer catetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases include arthritic conditions, demyelinating diseases. Such diseases include arthritic conditions, demyelinating cophoritis, autoimmune thyroiditis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, corhoric sensitivity disease, diseases militums faraves disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, disease, disease mellitums Graves disease, graft-versus-host disease, uidopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases, which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The gropperties of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which markers makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                     AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                           Claim 10; Page 14; 72pp; English
   WPI; 2000-317499/27
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Sequence 86 AA;

96 ------39 Gaps 30; 87.6%; Score 233; DB 3; Length 86; 62.8%; Pred. No. 2.3e-16; 0; Indels 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAK-----2; Mismatches 40 -----YKAEAAKAAAKEAYEA 56 54; Conservative Local Similarity Query Match Matches 8 요 ò 셤

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4. AAY82574 standard; peptide; 66 AA. 28-JUL-2000 AAY82574; AAY82574

ID AAY

AC AAA

AC AAA

XXX AAA

XXX AAA

XXX COP

DDE COP

COP

KW Gla

Gla

KW Gla

GRW ABB

KW HBB

KW HB

KW H

(first entry)

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified

WO200018794-A1

06-APR-2000

99WO-US022402. 24-SEP-1999;

98US-0101693P. 25-SEP-1998;

(YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; Gad A, WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY92571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer cactate related tetrapolymers. The polypeptides may also be used for actating and preventing immune diseases in a mammal. Autoimmune diseases cactate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroidmines, e.g. multiple sclerosis, crontact arthritis, osteoarthritis, autoimmune thyroidmines, e.g. multiples sclerosis, crontact cophoritis, autoimmune thyroidmines, e.g. multiples sclerosis, contact cophoritis, autoimmune thyroidmines, e.g. multiples sclerosis, disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic mysoedema, mysathenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated cophoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated cophoriamis nost disease, and delayed-type hypersensitivity. The properties which are analogous to glatiramer acetate molecules, which are analogous to glatiramer acetate molecules, which are an

Sequence 66 AA;

74.4%; Score 198; DB 3; Length 66; 80.3%; Pred. No. 5.9e-13; ive 2; Mismatches 1; Indels 10; Gaps Query Match
Best Local Similarity 80.3'

5

1 AKKYAKKEKAY--AKKAE-KAAK--KAEAKAY-KAAEAKKK----AEAKYKAEAAKAAAK 50

ò 셤 51 EAAYEA 56 ò

61 EAAYEA 66 셤

RESULT 5 AAY82577

AAY82577 standard; peptide; 109 AA.

AAY82577;

(first entry) 28-JUL-2000 Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

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treating and preventing immune diseases in a mammal. Autoimmune diseases
treating and preventing immune diseases in a mammal. Autoimmune diseases
treating and preventing immune diseases in a mammal. Autoimmune diseases

treating and preventing include arthritic conditions, demyelinating
diseases. Such diseases include arthritic conditions, demyelinating
diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid
arthritis, osteoarthritis, autoimmune baemolytic anaemia, autoimmune
cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, contact
cophoritis, autoimmune thyroiditis, autoimmune conditis, contact
cophoritis, pemphigus valabetes mellitus, Graves disease, Guillain-Barre's
snsitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's
syndrome, Hashimoto's disease, idiopathic myrosdema, myasthenia gravis,
c soriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated
mediated diseases which can be treated include host-versus-graft disease,
c polypeptides of the invention have defined molecular weights and physical
properties which are analogous to glatiramer accetate molecules, which
c makes them ideal for use as molecular weight markers
the invention are used as molecular weight markers for glatiramer
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Sequence 56 AA;

ö Gaps 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA 56 ; 0 100.0%; Score 266; DB 3; Length 56; 100.0%; Pred. No. 6.7e-20; 0; Indels 0; Mismatches Local Similarity 100. Les 56; Conservative Query Match Matches Š

AAY82575 standard; peptide; 77 AA

AAY82575;

(first entry) 28-JUL-2000 Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidabetic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified

WO200018794-A1

36-APR-2000

99WO-US022402. 24-SEP-1999;

98US-0101693P. 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Gad A, Lis D;

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English

AAY82571 to AAY82577 represent specifically claimed copolymer molecular

invention describes polypeticies (1) for determining the molecular weight invention describes polypeticies (1) for determining the molecular weight of a copolymer (2P), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer of the invention are used as molecular weight markers for glatizamer content of the invention are used as molecular weight markers for glatizamer of the invention and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include atthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid atthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thrombocytopania purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Gilliain-Barre's snaitivity disease, diabetes mellitus, Graves disease, Gilliain-Barre's snaitivity disease, hich can be treated include host-versus-graft disease, and delayed-type hypersensitivity. The groinsis of the invention have defined molecular weights and physical copypoprities which are analogous to glatizamer acetate molecules, which makes them ideal for use as molecular weight markers weight TV-marker polypeptides from the present invention. The present

Sequence 77 AA;

ä ----- AEAK 39 21; Gaps 92.3%; Score 245.5; DB 3; Length 77; 72.7%; Pred. No. 1.1e-17; ive 0; Mismatches 0; Indels 23 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK----56; Conservative Best Local Similarity Query Match Matches

1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKABEAKKKAKAEAKKYAKAAKAEKEYAAAEAK 60

77 40 YKAEAAKAAAKEAAYEA

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AAY82576 ID AAY8 RESULT 3

AAY82576 standard; peptide; 86 AA.

AAY82576;

(first entry) 28-JUL-2000

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

WO200018794-A1

06-APR-2000

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; Gad A,

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

December 14, 2004, 05:47:53 ; Search time 61.9072 Seconds (without alignments) 324.499 Million cell updates/sec Run on:

US-10-792-311-3

Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 23Sep04:* Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	2	Aay82575 Copolymer						Abu39221 Protein e	Abu28559 Protein e	Abb49123 Listeria	Abu32619 Protein e	Abu47123 Protein e	Abu44721 Protein e	Aar06446 Recombina	Abu27824 Protein e		Abu31397 Protein e	Abo67048 Klebsiell	Abg80418 Haemophil				Aay59044 Amino aci		Aau04289 Poly-Lys-
ΙΒ	AAY82573	AAY82575	AAY82576	AAY82574	AAY82577	AAY82572	ABU40185	ABU39221	ABU28559	ABB49123	ABU32619	ABU47123	ABU44721	AAR06446	ABU27824	ABU47848	ABU31397	ABO67048	ABG80418	AB023507	AAY82571	AAY98499	AAY59044	AAB45852	AAU04289
BB BB	м	٣	m	m	m	m	y	φ	9	Ŋ	9	9	9	N	9	9	9	7	ß	7	m	m	m	4	4
% Query Match Length	95	77	98	99	109	45	372	389	421	239	239	407	387	106	428	376	323	469	372	372	35	100	100	100	100
& Query Match	100.0	92.3	87.6	74.4	67.9	20.6	44.0	44.0	44.0	43.8	43.8	42.7	42.3	41.7	41.7	41.5	40.8	40.8	39.7	39.7	39.3	39.1	39.1	39.1	39.1
Score	266	245.5	233	198	180.5	134.5	117	117	117	116.5	116.5	113.5	112.5	111	111	110.5	108.5	108.5	105.5	105.5	104.5	104	104	104	104
Result No.		7	м	4	2	9	7	89	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

154 2 AAR06445 223 6 AB714928 361 7 ADF05105 347 6 ABU38313 347 6 ABU38313 347 6 ABJ18771 407 7 ABO80835 146 4 AAM25508 357 6 ABM67869 357 6 ABM67869 357 6 ABM67869 357 6 ABM67869 357 6 ABM67869 357 6 ABM67869 40 7 AAC30868 42 8 ABC71043 42 7 AAC71043 42 7 AAC71043 42 7 AAC71043 42 7 AAC71043 42 6 ABP57088 42 7 AAC71043 42 7 AAC71068		Adeloso4 Scinceura
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ALIGNMENTS

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosupressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; hememostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; draves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; permisis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3. Ä. AAY82573 standard; peptide; 56 (first entry) 28-JUL-2000 AAY82573; RESULT 1 AAY82573

WO200018794-A1.

06-APR-2000.

99WO-US022402. 24-SEP-1999; 98US-0101693P.

25-SEP-1998;

CO LTD. DEV (YEDA) YEDA RES & (TEVA-) TEVA PHARM

Lis D; Gad A, WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAV82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

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December 14, 2004, 05:47:53; Search time 72.962 Seconds (without alignments) 324.499 Million cell updates/sec
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version 5.1.6
- 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
GenCore (c) 1993
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Run on:

2002273 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 Minimum DB Maximum DB

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_23Sep04:* geneseqp2000s:* geneseqp2001s:* geneseqp1980s:* geneseqp1990s:* geneseqp2002s:* 2 6 4 5 9 7 8 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

uo	Copolymer	Copolymer	Copolymer	Copolymer	Copolymer	Protein e	Protein e	Protein e	Klebsiell	Recombina	Peptide #	Amino aci	Nucleic a	Poly-Lys-	Protein e	Protein e	Protein e	Protein e	Recombina	Protein e	Copolymer	Protein e	Pseudomon	Pseudomon	Haemophil
Description	Aay82574	Aay82575	Aay82576	Aay82577	Aay82573	Abu28559	Abu31397	Abu27824	Abo67048	Aar06445	Aay98499	Aay59044	Aab45852	Aau04289	Abu39221	Abu47123	Abu40185	Abu47848	Aar06446	Abu44721	Aay82572	Abu38313	Abj18771	Abo80835	Abg80418
QI QI	AAY82574	AAY82575	AAY82576	AAY82577	AAY82573	ABU28559	ABU31397	ABU27824	ABO67048	AAR06445	AAY98499	AAY59044	AAB45852	AAU04289	ABU39221	ABU47123	ABU40185	ABU47848	AAR06446	ABU44721	AAY82572	ABU38313	ABJ18771	ABO80835	ABG80418
DB	m	m	m	m	m	9	9	9	7	0	m	e	4	4	9	9	9	9	0	9	m	9	9	7	2
% Query Match Length DB	99	77	98	109	26	421	323	428	469	154	100	100	100	100	389	407	372	376	106	387	45	347	347	407	372
% Query Match	100.0	90.3	85.6	73.0	63.3	41.9	41.5	41.5	41.5	41.4	40.9	40.9	40.9	40.9	40.4	39.8	39.1	39.1	39.0	38.7	38.5	38.2	38.2	38.2	37.5
Score	313	282.5	268	228.5	198	131	130	130	130	129.5	128	128	128	128	126.5	124.5	122.5	122.5	122	121	120.5	119.5	119.5	119.5	117.5
Result No.	-	7	m	4	ß	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abo23507 Haemophil	Abm67869 Photorhab	Abu50266 Protein e	Abu42038 Protein e	Adf05105 Bacterial	Abp57088 Mouse MKP	Ada33882 Acinetoba	Abb49123 Listeria	Abu32619 Protein e	Aab20575 Mycobacte	Abg71044 Tumour ne	Aab95499 Human pro	Aau03592 Human DNA	Aab94309 Human pro	Abp69558 Human pol	Aay34055 M. tuberc	_	Abu34623 Protein e	Abu36893 Protein e	Aay82571 Copolymer
AB023507	ABM67869	ABU50266	ABU42038	ADF05105	ABP57088	ADA33882	ABB49123	ABU32619	AAB20575	ABG71044	AAB95499	AAU03592	AAB94309	ABP69558	AAY34055	AAY57353	ABU34623	ABU36893	AAY82571
7	9	9	ø	7	ø	9	Ŋ	9	m	Ŋ	4	4	4	Ŋ	7	~	9	9	m
372	357	388	336	361	452	214	239	239	205	80	198	279	467	467	214	214	214	214	35
37.5	37.4	37.4	36.7	36.6	36.4	36.3	35.6	35.6	35.3	35.0	34.7	34.7	34.7	34.7	33.9	33.9	33.9	33.9	33.7
117.5	117	117	115	114.5	114	113.5	111.5	111.5	110.5	109.5	108.5	108.5	108.5	108.5	106	106	106	106	105.5
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

glatitamer accetet, autoimmune disease, antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyrominetic; haemostatic; antipsoriatic; dermatory; antidabetic; thyrominetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4. Copolymer; molecular weight marker; TV-marker; immune disease; AAY82574 standard; peptide; 66 AA. (first entry) WO200018794-A1. Unidentified. 28-JUL-2000 AAY8257

99WO-US022402. 24-SEP-1999;

06-APR-2000.

98US-0101693P. 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Gad A, Lis D;

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

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cetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include either cell-mediated or antibody-mediated diseases. Such diseases include atthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cooporitis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoro's disease, idiopathic mycodema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
the invention are used as molecular weight markers for glatiramer
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Sequence 66 AA;

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AKKYAKKEKAYAKAKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK 60
                         Gaps
                         ö
  Length 66;
                        0; Indels
  100.0%; Score 313; DB 3; 100.0%; Pred. No. 6.9e-24;
                        0; Mismatches
                        66; Conservative
Query Match
Best Local Similarity
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                                                                                                                  61 EAAYEA 66
                        Matches
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AAY82575 standard; peptide; 77 AA. AAY82575; Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.

(first entry)

28-JUL-2000

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acctate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; hemostetic; antipsoriatic; dermatological; antidiabetic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; thrumatoid arthritis; crohn's disease; chronic immune thromboytopeania purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified

WO200018794-A1

06-APR-2000.

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998;

(YEDA) YEDA RES & DEV CO LTD (TEVA-) TEVA PHARM USA INC.

Lis D; Gad A, WPI; 2000-317499/27

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

```
AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides [1] for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatitamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases of treating and preventing immune diseases in a mammal. Autoimmune diseases of diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, outcommune thyroiditis, autoimmune baemolytic ansemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune thyroiditis, autoimmune thyroiditis, autoimmune thyroiditis, autoimmune thyroiditis, so canses, chabetes mellitus, Graves disease, Chon's Gisease, chronic immune thyroiditis, autoimmune wasthenia gravis, sonitatis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated.

Cophoritis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated.

Copolasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated.

Colaseases which can be treated include host-versus-graft disease, and delayed-type hypersensitivity. The most disease, and delayed-type hypersensitivity. The properties which have defined molecular weights and physical properties which an analogous to glatiramer acetate molecules, which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAYAK-----AKKAEAK-----AAKKAKAEAKKYAKAAKAEKKEYAAAEAK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.3%; Score 282.5; DB 3; Length 77; 84.4%; Pred. No. 8.4e-21; ive 0; Mismatches 1; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              properties which are analogous to glatiramer acetate makes them ideal for use as molecular weight markers
                            Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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65; Conservative
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Best Local Similarity
Matches 65; Conserv
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Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6. Copolymer; molecular weight marker; TV-marker; immune disease; 28-JUL-2000 (first entry)

AAY82576 standard; peptide; 86 AA.

RESULT 3

syndrome; psoriasis; glatizamer acetate, autoimmune disease, antiarchritic, neuroprotective, osteopathic; immunosuppressive; antithyroid; antinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified.

WO200018794-A1

99WO-US022402. 24-SEP-1999;

98US-0101693P 25-SEP-1998;

(YEDA) YEDA RES & DEV CO LTD.

(YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

99WO-US022402. 98US-0101693P.

24-SEP-1999; 25-SEP-1998;

06-APR-2000.

```
AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer cof the invention are used as molecular weight markers for glatiramer cactate related terrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases cactate related terrapolymers. The polypeptides may also be used for treating and preventing immune diseases include atther cell-mediated or antibody-mediated diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, contact disease, chronic immune thyroidmine, e.g. multiple sclerosis, contact coophoritis, autoimmune thyroidmine, graves disease, disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic mysocedema, myashhania gravis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, and delayed-type hypersensitivity. The properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
                                                                                                                                                                     Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                                                                                                                          Claim 10; Page 14; 72pp; English.
(TEVA-) TEVA PHARM USA INC
                                                                                                               WPI; 2000-317499/27
                                                         Lis D;
                                                      Gad A,
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Sequence 86 AA;

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1 AKKYAKKEKAYAKKAEKAAKAEAKAYKAABEAKKKAKAEAKKYAKAKAEKKEYAKAKAFAAAEAK 60
                                                               1 AKKYAKKEKAYAK----AKKAEAK-----AAKKAKAEAKKYAKAAKAEKKEYAAAEAK 49
                                       Gaps
                                    20;
           Length 86;
                                     1; Indels
           Score 268; DB 3;
Pred. No. 2.6e-19;
85.6%; Sco...
75.6%; Pred. No. ....
0; Mismatches
                                                                                                                        50 -----YKAEAAKAAAKEAAYEA 66
                                                                                                                                        65; Conservative
                        Local Similarity
           Query Match
                                                                                        셤
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                                                                                                                                                g
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RESULT 4

AAY82577 standard; peptide; 109 28-JUL-2000 (first entry) AAY82577;

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.

glatiramer acetate, autoimmune disease, antiarthritic; neuroprotective; osteopathic; immunosuppressive, antithyroid; antiinflammatory; antiinflammatory; antiinflammatory; antiinflammatory; thyromimetic; hemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; antianaemicyr condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thromboytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Copolymer; molecular weight marker; TV-marker; immune disease; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

WO200018794-A1

Unidentified AAY82577
IID AAY8
XX AC AAY8
XXX XXX
XXX COP
X

weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight TV-marker polypeptides (I) for determining the molecular weight and an an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer of the invention are used as molecular weight markers for glatiramer to determining the invention are used as molecular weight markers for glatiramer to determine the polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases is Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune tharoditis, autoimmune uveoretinitis, corbact schoolitis, autoimmune thrombocytopania purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Gilliain Barre's syndrome, Habhimoco's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated disease which can be treated include host-versus-graft disease, and delayed-type hypersensitivity. The grouperties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers to AAY82577 represent specifically claimed copolymer molecular Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases. Gaps 43; 73.0%; Score 228.5; DB 3; Length 109; 56.9%; Pred. No. 2.7e-15; ive 0; Mismatches 4; Indels 43 26 -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA 66 1 AKKYAKK-EKAYAKAKA------EAKAAKKA--Claim 10; Page 14; 72pp; English. 62; Conservative Query Match Best Local Similarity WPI; 2000-317499/27. Sequence 109 AA; Gad A, Matches 셤 ò

4 1 AKKYAKKAEKAYAKKAKAKAKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60 AAY82573 standard; peptide; 56 AA AAY82573

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3. (first entry) 28-JUL-2000

AAY82573;

Protein encoded by Prokaryotic essential gene #14086

```
AAY 82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer actactate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases of treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid diseases and inflammatory conditions, e.g. multiple sclerosis, contact coophoritis, autoimmune thyroidmune haemolytic anaemia, autoimmune coophoritis, autoimmune thyroidmune barenimis, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic mysocedema, myasthenia gravis, contact syndrome, Hashimoto's disease, idiopathic mysocedema, myasthenia gravis, permphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, conjunction have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which
Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, diabetes mellitus, Graves disease, Guillain Barre's syndrome, psoriasis, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                        pemphigus vulgaris; systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                     DEV CO LTD.
                                                                                                                                                                                                                                                                                                         98US-0101693P.
                                                                                                                                                                                                                                                            99WO-US022402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                     (YEDA ) YEDA RES & (TEVA-) TEVA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 56 AA;
                                                                                                                                                                WO200018794-A1
                                                                                                                                                                                                                                                                                                                                                                                                                          Gad A, Lis D;
                                                                                                                     Unidentified
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                                                              1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK
                        10;
  Length 56;
                        1; Indels
Score 198; DB 3;
Pred. No. 1.4e-12;
2; Mismatches 1;
 63.3%;
80.3%;
                      53; Conservative
Query Match
Best Local Similarity
                        Matches
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ABU28559 standard; protein; 421 AA. 26 61 EAAYEA 66 EAAYEA RESULT 6
ABU28559
ID ABU2
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AC ABU2
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DT 19-J ò

(first entry)

19-JUN-2003

ABU28559;

48 1 AKKYAKKEKAYAKAK-----KAEAKAAKKAKAEAKKYAK-----AAKAEKK-EYAAAEA 12; 16; Indels Conservative Local Similarity es 41; Conserv Best Loca Matches

The invention relates to an isolated nucleic acid comprising any one of the fall antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid of the nucleic acid, (2) a host cell containing the vector; (3) an isolated or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding oplypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding cell polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway required for proliferation, or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound sectivity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism; or (13) identifying the target of a compound that inhibits the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids are prequired for cellular proliferational New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MUPO at firmy howlpublished_pct_sequences Antisense; prokaryotic essential gene; cell proliferation; drug design. Zyskind JW; Xu HH; Length 421; Ohlsen KL, Forsyth RA, Score 131; DB 6; Pred. No. 4.9e-05; 9; Mismatches 16 Haselbeck R, Yamamoto R, Claim 25; SEQ ID NO 56483; 1766pp; English. Malone C, Carr GJ, 06-SEP-2001; 2001US-00948993. 25-0CT-2001; 2001US-0342923P. PEBS-2002; 2002US-0072851. 06-MAR-2002; 2002US-0362699P. 21-MAR-2002; 2002WO-US009107 21-MAR-2001; 2001US-00815242. 41.9%; (ELIT-) ELITRA PHARM INC. Zamudio C, Trawick JD, 2003-029926/02 N-PSDB; ACA32429 Sequence 421 AA; WO200277183-A2 03-OCT-2002 Query Match ų, Wang Wall 셤

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(1) a vector comprising a proincerably linked to the nucleic acid cacid (1) a vector comprising a promoter operably linked to the nucleic acid cacid; (2) a host cell containing the vector; (3) an isolated continued a polypeptide whose expression is inhibited by the antisense uncleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or the that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological contains a gene product or that has an activity gainst a biological pathway in which a proliferation-required gene or its gene product is oversive compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound it activity; (11) a culture compound that inhibits proliferation of compound its crivity; (11) aculture compound that inhibits proliferation of the strains is present in a culture or collection of the which each of the strains is present in a culture or collection of the which each of the strains is present in a culture or collection of the proliferation of an organism. The antisense nucleic acids required corrections or screening for homologous nucleic acids required corrections. The adultat promoter acids are useful for cellular proliferation in cells other candidate molecules for rational cert equired for proliferation in cells other sequence is encoded by one of required for proliferation in cells other enemediate.
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Xu HH;
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Forsyth RA,
                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #16924.
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Yamamoto R,
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                                                                                                                   ABU31397 standard; protein; 323 AA.
                             Malone C,
Carr GJ,
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25-OCT-2001; 2001US-034223P.
PEBS-2002; 2002US-0072851.
06-MAR-2002; 2002US-0362899P.
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               KYKAEAAKAAAKEAAYEA
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                                                                                                                                                                                                                                                                   Klebsiella pneumoniae.
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Trawick JD,
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ID ABU
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11 a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8)
                                                                                                                                                                                                                                                                                                                                                       screening
the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Xu HH;
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for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                    Length 323;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #13351.
                                                                                                                                                                                                    Score 130; DB 6;
Pred. No. 4.6e-05;
6; Mismatches 18
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Yamamoto R,
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Carr GJ,
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25-0CT-2001; 2001US-0342923P.
PEBS-2002; 2002US-00072851.
06-MAR-2002; 2002US-0072851.
                                                                                                                                                                                                 cn 41.5%;
1 Similarity 57.7%;
41; Conservative 6
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140 QKAAAEKAAAE 150
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Trawick JD,
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                                                                                                                                               Sequence 323
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                                                                                                                                                                                                    Query Match
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Wall D,
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pathway in which a proliferation required possession of the broadcast pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts, (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK 60
  identifying a gene required for cellular proliferation or the biological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.5%; Score 130; DB 6; Length 428; 56.1%; Pred. No. 6.2e-05; ive 11; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Conservative
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The invention describes a new isolated nucleic acid encoding a Klebsiella pheumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression
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N-PSDB; ABD00619.
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ABO67048

ABO670
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for improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue cocurs between the Protein A and rCOP-1 sequences, originating from the fusion protein. rCOP-1-77 contains oligonucleotide may be cleaved from the fusion protein. rCOP-1-77 contains oligonucleotide duplexes incoding the following segments: YKK, EAE, KAK, AAK, and AAA. The N-terminal alamine residue is left behind following CNBr cleavage of the fusion protein. The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain manno acids. See also AAQ05665. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                    ų,
                                                                                                                                                                                                            Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis.
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vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                       1 AKKYAKKEKAYAKA---KKAEAKAAKKAKAEAKKYA--KAAKAEKKEYAAAE-AKYKAEA
                                                                                                                                                    6; Gaps
                                                                                                               Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant copolymer 1-77, myelin basic protein analogue.
                                                                                                           Score 130; DB 7; Length 46
Pred. No. 6.9e-05;
6; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                             AAR06445 standard; protein; 154 AA.
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90US-00473845.
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                                                                                                             Query Match
Best Local Similarity 57.7%;
Matches 41; Conservative
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290 QKAAAEKAAAE 300
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N-PSDB; AAQ05664.
                                                                           Sequence 469 AA;
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07-FEB-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP383620-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR06445;
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                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                AAR06445
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The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36633-A36622 and peptide sequences AAA98456-Y98500 are used in the construction of the transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for transporter systems are also used to create transport and infection. The transporter systems are also used to create transport and infection. The transporter systems are also used to create transport and infection of the man carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting calls in vitro to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from
                                                                          ω,
                                                                                                             ---KKYAKAAKAEKKEYAAAEAKYKA 52
                                                                                                                                   System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent.
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.
                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endosomes, without requiring endosomal or lysosomal degradation
                                   41.4%; Score 129.5; DB 2; Length 154; 48.8%; Pred. No. 2.3e-05; ive 7; Mismatches 17; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #10 used in nucleic acid transporter system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sparrow J, Cristiano RJ, Woo SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Col 125-128; 108pp; English.
                                                                                                             2 KKYAKKEKAYAKAKKAEAKAAKKAKAEA-
                                                                                                                                                                                                                                                                                                                       AAY98499 standard; peptide; 100 AA
                                                                                                                                                                                                                         98 EAEEAEYKKYKKKÄKKÄKYK 117
                                                                                                                                                                                     53 EAAKA-----AAKEAAYE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-00167641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92US-00855389
93WO-US002725
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                    Local Similarity 48.8
nes 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-281993/24.
 Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6033884-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                            AAY98499;
                                   Query Match
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40.9%; Score 128; DB 3; Length 100; 62.7%; Pred. No. 2.1e-05;

Best Local Similarity

Query Match

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The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moving or initiating movement through a nuclear membrane; and/or c (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytoplasm of the cell. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting specific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells. The NTS can be used in vitro with tissue culture cells. The yes agent within the NTS avoids the problem of endosomal/lysosommal
 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
                               1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK 56
                                              4; Gaps
                                                                                                                                                                                                                                                                                                                              Nucleic acid transport system; NTS; cell surface receptor; cytosis; nuclear membrane; lysis moiety; transgenic animal; human disease; nucleic acid delivery; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith LC;
 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sparrow J,
                                                                                                                                                                                                                                                                                                    Amino acid polymer seq ID NO: 64 of US5994109.
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Col 123-124; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                       AAY59044 standard; peptide; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BAYU ) BAYLOR COLLEGE MEDICINE.
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                                                                                                                                                                                                                                                                    (first entry)
 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cristiano RJ,
                                                                                          57 AAAKEAA 63
                                                                                                                          62 AKAKAKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-038262/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 100 AA;
                                                                                                                                                                                                                                                                      07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-1992;
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14-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                     AAY59044;
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 Matches
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Gaps

4;

Indels

16;

5; Mismatches

42; Conservative

Matches

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This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding concovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid. The nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor cupressors, viral antigens, parasitic antigens, and bacterial antigens. The transporter system uses lyaks agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems
                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                           oncogene;
                                                                        99
                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene tumor antigen; tumor suppressor; viral antigen; parasitic antigen; bacterial antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors.
                                                                                            1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK
                                       Gaps
                                       4
                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid transporter system peptide ligand SEQ ID NO 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WOO SLC
   Length 100;
                                    16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith LC,
40.9%; Score 128; DB 3;
62.7%; Pred. No. 2.1e-05;
ive 5; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Col 125-126; 105pp; English.
                                                                                                                                                                                                                                                                AAB45852 standard; protein; 100 AA.
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93WO-US002725.
93US-00167641.
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                                                                                                                                                                                                                                                                                                                                    (first entry)
                  Local Similarity 62.7 tes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-049093/06.
                                                                                                                                          57 AAAKEAA 63
                                                                                                                                                                           AKAKAKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-1995;
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19-MAR-1993;
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                                                                                                                                                                                                                                                                                                  AAB45852;
   Query Match
                   Best Loca
Matches
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Score 128; DB 4; Length 100; Pred. No. 2.1e-05;

40.9%;

Query Match Best Local Similarity

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The sequence represents poly-Lys-Ala, used to bind nucleic acid in a nucleic acid transporter system. The nucleic acid transporter system were nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules, lysis agents and spacer molecules are used in nucleic acid transporter systems to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK 56
                           61
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                                                                                                                                                                                                                                                                               Nucleic acid transport, cytosis; ligand; lysis agent; spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK
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    100
    /note= "Lys-Ala in positions 3-100 may be present absent"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Match 40.9%; Score 128; DB 4; Length 100; Local Similarity 62.7%; Pred. No. 2.1e-05; es 42; Conservative 5; Mismatches 16; Indels
                                                                                                                                                                                                                                                   Poly-Lys-Ala used in nucleic acid transporter system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Col 131; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                               AAU04289 standard; peptide; 100 AA.
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93US-00167641.
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                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-365933/38.
                                                          63
                                                                                    62 AKAKAKA 68
                                                         57 AAAKEAA
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                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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14-DEC-1993;
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                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                                                                                                                            AAU04289;
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Matches
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Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                 Protein encoded by Prokaryotic essential gene #24748.
                                                                                                                                                                                       Haselbeck R,
Yamamoto R,
                              ABU39221 standard; protein; 389 AA.
                                                                                                                                                                                       Malone C,
Carr GJ,
                                                                                                                                        21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                                                                            21-MAR-2002; 2002WO-US009107
                                                                                                                                                           2002US-00072851.
                                                                                                                                                                06-MAR-2002; 2002US-0362699P
                                                     19-JUN-2003 (first entry)
                                                                                                                                                                            (ELIT-) ELITRA PHARM INC.
                                                                                          Pasteurella multocida.
                                                                                                                                                                                        Zamudio C,
Trawick JD,
                                                                                                                                                                                                         2003-029926/02
 AKAKAKA 68
                                                                                                                                                                                                               N-PSDB; ACA43091
                                                                                                     WO200277183-A2
                                                                                                                                                          08-FEB-2002;
                                                                                                                03-OCT-2002.
                                          ABU39221;
62
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                                                                                                                                                                                        Wang
Wall
                   RESULT 15
                                                                                                                                                                                                          WPI:
                         ABU3922
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Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

the first and interaction where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular cross proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway to proliferation, (7) identifying a compound that influences the activity of pathway in which the test compound that proliferation of an identifying a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or compound that inhibits proliferation of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational contraining proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational contragined for proliferation in cells other than S. arrens; crequired for proliferation in cells other than S. arrens; crequired for proliferation in cells other than S. arrens; crequired for proliferation in cells other than S. arrens; crequired for this prosential genes. Note: The sequence data for this screening The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. Claim 25; SEQ ID NO 67145; 1766pp; English.

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                                                                                                                                                                          1 AKKYAKKEKAYAKAK-----KAEAKA---AKKAKAEAKKYAKAAKAEKKEYAAAEAKYK 51
patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                            Gaps
                                                                                                                            15;
                                                                                           Length 389;
                                                                                                                            Indels
                                                                                                .,
                                                                                           Query Match 40.4%; Score 126.5; DB 6; Best Local Similarity 52.0%; Pred. No. 0.00012; Matches 39; Conservative 9; Mismatches 12;
                                                                                                                                                                                                                                                     243 AEKAKADAEAAQRKA 257
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                                                                                                                                                                                                                       52 AEAAKAAAKEAAYEA
                                                                 Sequence 389 AA;
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December 14, 2004, 05:52:22 ; Search time 163.747 Seconds (without alignments) 143.965 Million cell updates/sec
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(cgn2 6/ptodata/1/pubpaa/DCT_NEW PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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313
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                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Sequence 4, Appli	Sequence 5, Appli	Sequence 6, Appli	Sequence 7, Appli	Sequence 3, Appli	Sequence 56483, A	Sequence 59321, A	Sequence 55748, A	Sequence 67145, A	Sequence 75047, A	Sequence 68109, A	Sequence 75772, A	Sequence 72645, A
SUMMARIES			ID	US-09-816-989A-4	US-09-816-989A-5	US-09-816-989A-6	US-09-816-989A-7	US-09-816-989A-3	US-10-282-122A-56483	US-10-282-122A-59321	US-10-282-122A-55748	US-10-282-122A-67145	US-10-282-122A-75047	US-10-282-122A-68109	US-10-282-122A-75772	US-10-282-122A-72645
			DB	6	φ	σ	σ	σ	15	15	15	15	15	15	15	15
		Query	Length	99	77	98	109	99	421	323	428	389	407	372	376	387
	æ	Query	Match	100.0	90.3	85.6	73.0	63.3	41.9	41.5	41.5	40.4	39.8	39.1	39.1	38.7
			Score	313	282.5	268	228.5	198	131	130	130	126.5	124.5	122.5	122.5	121
	,	Result	No.	1	7	m	4	S	9	7	æ	σ	10	11	12	13

61 EAAYEA 66 ||||||

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Sequence 2, Appli Sequence 120, App Sequence 66237, A Sequence 16, Appli Sequence 16, Appli Sequence 5, Appli Sequence 5, Appli Sequence 10710, A Sequence 20, Appli Sequence 20, Appli Sequence 27, Appli Sequence 62547, A Sequence 62547, A Sequence 6121, Appli Sequence 198446, Sequence 198446, Sequence 521, Appli Sequence 52, Appli Sequence 51, Appli Sequence 51, Appli Sequence 51, Appli Sequence 51, Appli	
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1110 1110 1111 1111 1111 1111 1111 111	103.5 103 103 103 102.5
1 1 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0	144444 112644

ALIGNMENTS

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APPLICANT: Gad, Alexander
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
CURRENT APPLICATION NUMBER: US/09/0101, 693
PRIOR FILING DATE: 1090-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VORISION 3.1
SEQ ID NOS: 7
SOFTWARE: PATENTIN VORISION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 313; DB 9; Length 66; 100.0%; Pred. No. 7.6e-22; tive 0; Mismatches 0; Indel8
                  Sequence 4, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
US-09-816-989A-4
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Matches
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKA
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKA
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Petentin version 3.1
SEQ ID NO 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKET TITLE OF INVENTION: AND FOR THERAPEUTIC USE CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT APPLICATION NUMBER: 60/101,693 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR RILING DATE: 1999-09-25 PRIOR RILING DATE: 1999-09-24 SPRIOR RILING DATE: 1999-09-24 SPRIOR FILING DATE: 1999-09-24 SPRIOR FILING DATE: 1999-09-34 SPRIOR FILING DATE: 1999-09-34 SPRIOR FILING DATE: 1999-09-24 SPRIOR FILING DATE: 19
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAABAKKKAKAEAKKYAKAAKAKEKKEYAABAK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 73.0%; Score 228.5; DB 9; Best Local Similarity 56.9%; Pred. No. 7.2e-14; Matches 62; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKK-EKAYAKAKKA------EAKAAKKA-
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                                                                                                                                                                           61 УКАЕЛАККАЎКАЁЛАКАЛАКЕЛАЎЕЛ 86
                                                                                                             50 -----YKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09816989A Patent No. US20020115103A1
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
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                                                                                                                                                                                                                                                                                                                         US-09-816-989A-7
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US-09-816-989A-3
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 00/101,693
PRIOR FILING DATE: 1999-09-25
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
FILLE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 06/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTION NUMBER: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTION VERSION 3.1
SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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Pred. No. 5.6e-19;
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Pred. No. 1.3e-17;
0; Mismatches 1; Indels
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                                                                                                                                                                    Sequence 5, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
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Patent No. US20020115103A1
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Local Similarity 84.4%;
hes 65; Conservative C
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SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 77
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ORGANISM: Artificial Seguence
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Best Local Similarity 75.6%;
Matches 65; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
   61 EAAYEA
                                                                                                      RESULT 2
US-09-816-989A-5
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US-09-816-989A-6
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Matches
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1 AKKYAKKEKAYAK-----AKKAEAK-----AAKKAKAEAKKYAKAAKAEKKEYAAAEAK 49

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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITRA.0347

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PLICATION NUMBER: 60/200,727

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-10-29

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 55748, Application US/10282122A
; Publication No. US20040029129A1
; GPUBRAL INFORMATION:
APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
                                                                                                                                                    ; Sequence 59321, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
   194 KKKAEAAEAAAEAKKA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Klebsiella pneumoniae US-10-282-122A-59321
                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                        Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                Ohlsen, Kari
Zyskind, Judith
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Matches 41; Conserva
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                                                                                                                                US-10-282-122A-59321
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APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT PILING DATE: 2003-02-20
RIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-29
PRIOR PILING DATE: 2001-12-29
PRIOR PILING DATE: 2001-02-09
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                                                                                                                             1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK 60
                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 12;
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th 63.3%; Score 198; DB 9; Length 56; Similarity 80.3%; Pred. No. 2.2e-11; 53; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 56483, Application US/10282122A Publication No. US20040029129A1
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Yamamoto, Robert
Forsyth, R
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Best Local Similarity 52...
Best Local 41; Conservative
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                       Best Local Similarity
Matches 53; Conserv
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EAAYEA 56
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   Query Match
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1 AKKYAKKEKAYAKAK-----KAEAKA----AKKAKAEAKKYAKAAKAEKKEYAAAEAKYK 51
                                  APPLICANT: Xu, H. TILLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen, Kari
29skind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Best Local Similarity 52.0
Matches 39; Conservative
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APPLICANT:
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FRICH APPLICATION NUMBER: 60/191,078
FRICH APPLICATION NUMBER: 60/206,848
FRICH APPLICATION NUMBER: 60/207,727
FRICH APPLICATION NUMBER: 60/207,727
FRICH APPLICATION NUMBER: 60/207,727
FRICH APPLICATION NUMBER: 60/230,335
FRICH APPLICATION NUMBER: 60/230,347
FRICH APPLICATION NUMBER: 60/230,347
FRICH APPLICATION NUMBER: 60/245,578
FRICH APPLICATION NUMBER: 60/253,625
FRICH APPLICATION NUMBER: 60/253,625
FRICH APPLICATION NUMBER: 60/253,625
FRICH APPLICATION NUMBER: 60/257,931
FRICH APPLICATION NUMBER: 60/257,931
FRICH APPLICATION NUMBER: 60/267,636
FRICH APPLICATION NUMBER: 60/267,636
FRICH APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.5%; Score 130; DB 15; Length 428; 56.1%; Pred. No. 0.00032; ive 11; Mismatches 16; Indels
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Yaskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Enterobacter cloacae US-10-282-122A-55748
                     Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
                                                                                                                       Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 56.11
Matches 37; Conservative
Malone, Cheryl
                                                                                                  Daniel
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US-10-282-122A-67145
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LENGTH: 428
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1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKA--EAAKAA 58
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Frior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 69109
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 75772
LENGTH: 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.1%; Score 122.5; DB : 51.5%; Pred. No. 0.0014; iive 10; Mismatches 18
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
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; ORGANISM: Pseudomonas putida
US-10-282-122A-68109
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Yamamoto, Robert
Forsyth, R.
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Matches 35; Conservative
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205 AEDAKKKA 212
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
RIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
39.8%; Score 124.5; DB 15; Length 407;
Best Local Similarity 47.8%; Pred. No. 0.00097;
Matches 43; Conservative 6; Mismatches 10; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 AAAEAKYKAEAA-----KAAAKEAA 63
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Carlos
APPLICANT: Malone, Carlos
APPLICANT: Malone, Cherl
APPLICANT: Alone, Carlos
APPLICANT: Alone, Carlos
APPLICANT: Alone, Judith
APPLICANT: Obleen, Kari
APPLICANT: Carr, Grant
APPLICANT: Travick, John
APPLICANT: Travick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Porsyth, R.
    PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/24,578
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-09
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/26,636
PRIOR APPLICATION NUMBER: 60/26,636
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-10-282-122A-75047
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LENGTH: 407
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US-10-127-032-120
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US-09-816-989A-2
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PRIOR PILLING DATE: 2000-03-21
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PRIOR PILLING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/200, 848
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/200, 727
PRIOR PILLING DATE: 2000-09-06
PRIOR PILLING DATE: 2000-09-09
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PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR PILLING DATE: 2000-10-23
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PRIOR PILLING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/267, 931
PRIOR PILLING DATE: 2001-02-09
PRIOR PILLING DATE: 2001-02-09
PRIOR PILLING DATE: 2001-02-09
PRIOR PILLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269, 308
PRIOR PILLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/269, 308
PRIOR PILLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269, 308
PRIOR PILLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269, 308
PRIOR PILLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269, 308
PRIOR PILLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269, 308
PRIOR PILLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269, 308
PRIOR PILLING DATE: 2001-02-16
PRIOR PILLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269, 308
PRIOR PILLING DATE: 2001-02-16
PRIOR PILLING DATE: 2001-02-10
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APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                      Gaps
                                                                                                                                                                                  21;
                                                                                                              Length 376;
                                                                                                                                                                                  13; Indels
                                                                                                  Score 122.5; DB 15;
Pred. No. 0.0014;
4; Mismatches 13;
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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Publication No. US20040029129A1
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1 LOCATION: (303) .. (303)

CTHER INFORMATION: X=any amino acid
US-10-282-122A-72645
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ORGANISM: Salmonella paratyphi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                  ch 39.1%;
il Similarity 51.3%;
40; Conservative
; ORGANISM: Salmonella typhi
US-10-282-122A-75772
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OTHER INFORMATION: X=any
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NAME/KEY: MISC_FEATURE
                                                                                                      Query Match
Best Local Similarity
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LENGTH: 387
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Sequence 2. Application US/09816989A

Factor No. US20020115103A1

GENERAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: Gad, Doris

TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REPRENEUR: 2609/6007-A-PCT-US

CURRENT FILING DATE: 1998-09-25

FRIOR PILING DATE: 1998-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PALENTIN VERSION 3.1

SEQ ID NO 2

LENGTH: 45
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Publication No. US20030113742A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Whiteley, Marvin
APPLICANT: Bangera, M. Gita
APPLICANT: Lory, Stephen
APPLICANT: Greenberg, Everett Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: METHODS AND COMPOSITION OF
TITLE OF INVENTION: US/10/12,032
CURRENT PLING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,190
PRIOR APPLICATION NUMBER: US 60/344,142
PRIOR PILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 170
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 120
LENGTH DATE: D
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Query Match
38.7%; Score 121; DB 15; Length 387;
Best Local Similarity 53.0%; Pred. No. 0.0019;
Matches 44; Conservative 6; Mismatches 15; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 AKKKADARRAKAAADAKKKAAAE 253
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ORGANISM: Artificial Sequence
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Query Match 38.2%; Score 119.5; DB 14; Length 347; Best Local Similarity 51.5%; Pred. No. 0.0024; Matches 34; Conservative 7; Mismatches 22; Indels 3; Gaps
US-10-127-032-120
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58 AAKEAA 63 ||::|| 215 AARKAA 220 \$ a \$ a

Search completed: December 14, 2004, 06:59:41 Job time : 163.747 secs

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Sequence 64, Appl
Sequence 64, Appl
Sequence 64, Appl
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Sequence 2, Appl
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Sequence 29581, A
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5169, Ap
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Sequence 7, Appli
Sequence 3, Appli
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            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-405-743A-7
US-09-405-743A-3
US-09-405-743A-3
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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1 AKKYAKKEKAYAKAYAKAAKAAKAAKAAKAAKAAAK
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Sequence 5, Application US/09405743A

Patent No. 651433B

GENERAL INFORMATION:

APPLICANT: Yeda Research and Development Co., Ltd.

TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS

FILE REPERENCE: 60807-A

CURRENT APPLICATION NUMBER: US/09/405,743A

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 77

TYPE: PRT

ORGANISM: Artificial Sequence
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Patent No. 6514938
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL APPLICANT: VEGA Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
TITLE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 66
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: PEPTIDE
US-09-405-743A-4
                   US-09-115-746-2

US-09-115-746-2

US-09-216-894-8

US-09-218-796A-26989

US-09-248-796A-26989

US-09-248-796A-26122

US-08-216-894-10

US-08-516-894-10

US-08-518-925-33

US-08-538-092-911

US-08-714-741-42

US-08-714-741-42

US-08-529-055-35

US-08-529-055-35

US-08-529-055-35

US-08-112-741-40

US-08-529-055-35

US-08-112-741-40

US-08-112-949-4

US-08-072-070-4
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100.0%; Score 313; DB 4; Best Local Similarity 100.0%; Pred. No. 1.1e-23; Matches 66; Conservative 0; Mismatches 0;
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61 EAAYEA
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RESULT 5
US-09-405-743A-3
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                    SYNTHETIC
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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FLE REPERBRICE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 86
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APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION:
GENERAL SEPERATION:
GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REPERENCE: 60807-4
CURRENT APPLICATION UNBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 109
                                                                                                                                   1; Indels 11;
                                                                                        Score 282.5; DB 4; Length 77;
Pred. No. 1.1e-20;
0; Mismatches 1; Indels 1:
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                OTHER INFORMATION: Description of Artificial Sequence: COTHER INFORMATION: PEPTIDE US-09-405-743A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: DESCRIPTION Of Artificial Sequence:
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-7
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; OTHER INFORMATION: PEPTIDE
US-09-405-743A-6
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09405743A Patent No. 6514938 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09405743A Patent No. 6514938
                                                                                                                                                                                                                                                   YKAEAAKAAAKEAAYEA 66
                                                                                                                                                                                                                                                                                      61 YKAEAAKAAKEAAYEA 77
                                                                                        Query Match
Best Local Similarity 84.4%;
Matches 65; Conservative (
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US-09-405-743A-6
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US-09-405-743A-7
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FEATURE:
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Sequence 1356, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: GALY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489,039A
TITLE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 1090-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
SEQ ID NO 13565
LENGTH: 469
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                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.3%; Score 198; DB 4; Length 56;
Best Local Similarity 80.3%; Pred. No. 1e-12;
Matches 53; Conservative 2; Mismatches 1; Indels 10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09405743A
| Sequence 3, Application US/09405743A
| Patent No. 6514938
| GENERAL INFORMATION:
| APPLICANIT: Veda Research and Development Co., Ltd.
| TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
| FILE REFERENCE: 60807-A
| CURRENT PAPLICATION NUMBER: US/09/405,743A
| CURRENT FILIND DATE: 1999-09-24
| NUMBER OF SEQ ID NOS: 7
| SEQ ID NO 3
| SEQ ID NO 3
| LENGTH: 56
                                                                                                                                                                                                                                  26 -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA 66
  Length 109;
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                                                      Indels
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; OTHER INFORMATION: PEPTIDE
US-09-405-743A-3
Score 228.5; DB 4;
Pred. No. 2.4e-15;
0; Mismatches 4;
                                                                                                     1 AKKYAKK-EKAYAKAKKA-----EAKAAKKA---
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US-09-489-039A-13565
Query Match 73.0%;
Best Local Similarity 56.9%;
Matches 62; Conservative
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                               62 AKAKAKA 68
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                                                                                                                       RESULT 8
US-08-167-641C-64
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   1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK 56
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US-08-460-890A-64

Sequence 64, Application US/08460890A

Patent No. 5394109

GENERAL INFORMATION

APPLICANT: Smith, Louis C.

APPLICANT: Cristiano, Richard J.

APPLICANT: Cristiano, Richard J.

APPLICANT: Cristiano, RICHARD OF USE

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: 631 West Fifth Street

COUNTRY: U.S.A.

ZILE 900712-08

COUNTRY: U.S.A.

ZILE 900712-08

COUNTRY: U.S.A.

ZILE 900712-08

COUNTRY: U.S.A.

ZILE 100 WINDER: 100 WINDER: 0.0

COUNTRY: U.S.A.

SOFTWARE: FastSEQ for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,890A

FILING DATE: December 14, 1993

APPLICATION NUMBER: 927/US31/02725

FILING DATE: MARCH 20, 1993

ATTORNEY/PRICE MARCH 19, 1933

APPLICATION NUMBER: 33.327

REGISTRATION NUMBER: 33.327

REGISTRATION NUMBER: 33.327

RESTSTRANCE/DOCKET NUMBER: 33.
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40.9%; Score 128; DB 2; Length 100;
Best Local Similarity 62.7%; Pred. No. 9.9e-06;
Matches 42; Conservative 5; Mismatches 16; Indels
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TYPE: amino acid
STRANDEDNESS: single
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290 QKAAAEKAAAE 300
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MOLECULE TYPE: peptide
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RESULT

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GENERAL INFORMATION:
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Sequence 64, Application US/08460971A

Sequence 64, Application US/08460971A

Patent No. 6150168

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Gottchalk, Louis C.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDERSS:
ADDERSSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: 603 West Fifth Street
STREET: Galifornia
COUNTY: Los Angeles
STATE: California
COUNTY: U.S.A.
ZIPE: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 18M Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
COMPUTER: IBM Compatible
OPERATION NUMBER: US/08/460,971A
FILING DATE: June 5, 1995
APPLICATION NUMBER: 07/855,389
FILING DATE: March 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
ATTING DATE: March 19, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Lys Ala" in positions 3 to 100 may be present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
40.9%; Score 128; DB 3; Length 100;
Best Local Similarity 62.7%; Pred. No. 9.9e-06;
Matches 42; Conservative 5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 312/063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELERA: (57-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
COTHER INFORMATION:
US-08-460-971A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 AAAKEAA 63
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US-08-462-040-64
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; Sequence 64, Application US/08462040; Patent No. 6177554

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Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: YeaR Research and Development Co., Ltd.
ITILE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.9%; Score 128; DB 3; Length 100; 62.7%; Pred. No. 9.9e-06; tive 5; Mismatches 16; Indels
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FEASTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTEM: IBM P.C. DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3:" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64: SEQUENCE CHARACTERISTICS: LENGTH: 100 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 62.77
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 AAAKEAA 63
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US-09-405-743A-2
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Sequence 5390, Application US/09543681A

Sequence 5390, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION:

DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

TITLE OF INVENTION:

OURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR PAPLICATION NUMBER: US 60/128,706

PRIOR PAPLICATION NUMBER: US 60/128,706

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 5390

LENGTH: 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 KAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AKAAAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                      COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.5%; Score 117.5; DB 3
65.5%; Pred. No. 5.6e-05;
tive 5; Mismatches 11
                                                                                                                                                                                                                                                                               PRIOR APPLICATION: 51-7
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 60/032,436
FILING DATE: 18 -DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: SUllivan, Sally A.
REGISTRATION NUMBER: 32.064
REFERENCE/DOCKET NUMBER: 33-95
TELEPHONE: 303-499-8080
TELEPHAX: 303-499-8080
TELEPHAX: 303-499-8080
TELEPHAX: 303-499-8080
TELEPHAX: 50-8080
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS: not relevant
not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 53.03
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 36; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 KAAAKE 61
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US-08-993-008A-6
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                                                                          80303
                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: UMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAK---KEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKA 57
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                          ) OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC; OTHER INFORMATION: PEPTIDE
US-09-405-743A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 38.2%; Score 119.5; DB 4; Length 407; Best Local Similarity 51.5%; Pred. No. 0.00027; Matches 34; Conservative 7; Mismatches 22; Indels 3
                                                                                                                                                                                                                                                                                                                                      38.5%; Score 120.5; DB 4; Length 45; nlarity 71.1%; Pred. No. 2.3e-05; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                        29 AKKYAKAAKAE--KKEYAAAEAK----YKAEAAKAAAKEAAYEA 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polycationic Oligomers
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 29581, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08993008A
Patent No. 6153596
GENERAL INFORMATION:
APPLICANT: Liotta, Dennis C.
APPLICANT: Petros, John A.
APPLICANT: Wey, Shlow-dyi
APPLICANT: Karr, Joan F.
APPLICANT: Pell Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29581
                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PO NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: ADDRESSE: Greenlee,
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||::||
275 AARKAA 280
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US-08-993-008A-6
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RESULT 15
US-09-328-352-5169
i Sequence 5169, Application US/09328352
j Patent No. 6562958
j General INFORMATION:
i APPLICANT Gary L. Breton et al.
i TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
i TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
i CURRENT FILING DATE: 1999-06-04
i CURRENT FILING DATE: 1999-06-04
i NUMBER OF SEQ ID NOS: 8252
i SEQ ID NO 5169
i LENGTH: 214
i TYPE: PRT
i ORGANISM: Acinetobacter baumannii
i ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 36.3%; Score 113.5; DB 4; Length 214; Best Local Similarity 51.4%; Pred. No. 0.00052; Matches 37; Conservative 9; Mismatches 17; Indels 9.
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Search completed: December 14, 2004, 05:50:17 Job time : 18.6618 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

December 14, 2004, 05:47:53 ; Search time 17.7068 Seconds (without alignments) 418.411 Million cell updates/sec Run on:

US-10-792-311-5 366 1 AKKYAKKEKAYAKKAEKAAK......BAKYKAEAAKAAAKEAAYEA 77

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

, see	Description	tolA protein - Esc	membrane spanning		tolA protein [impo	Tola protein PA097		probable erythrocy	ᅼ	ve pr	histone H1 - Chlam	R27-2 protein - Tr	cytosolic repetiti	TolA colicin impor	sperm tail-specifi	probable hupB - My	histone H1-beta, e	mst101-1 protein -	H1-6	histone H1, gonada	zuotin - yeast (Sa	histone H1 - sea u	histone H1.10 - ch	hypothetical prote	hypothetical prote	hypothetical prote	н	H1 (clor	H1-II	histone H1 - rainb
<u> </u>	TD	JV0057	F90725	G85576	AG0592	E83525	G64064	T09127	A25550	E60110	859589	T30296	A44993	AC0138	S51364	G70673	A28100	S34153	A26721	HSUR1P	S25194	509388	A28456	T17698	AE1689	AE1317	B43592	T06241	JN0748	HSTRIR
9	9 1	7	N	~	~	7	~	7	7	7	~	7	7	~	~	~	~	~	N	н	~	~	N	~	~	7	~	~	~	7
% Query Match Ionath		421	394	394	376	347	372	1701	210	219	231	1128	328	388	1390	214	211	344	217	248	433	206	220	311	243	239	384	284	241	206
Query	March	41.1	40.4	40.4	39.9	38.7	38.5	37.7	37.2	36.7	36.7	36.6	36.3	35.7	35.5	35.4	35.1	34.8	34.7	33.6	έ,	٠	•	33.5	٠	•	33.2	32.9	32.4	32.2
Š	Score	150.5	148	148	146	141.5	141	138	136	134.5	134.5	134	133	130.5	130	129.5	128.5	127.5	127	123	\sim	122.5	122.5	122.5	122	121.5	121.5	120.5	118.5	118
Result	. PO.	-	7	e	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT 2 F90725

probable translati	cgcr-4 protein - C	histone H1 (clone	histone H1.11L - c	hypothetical prote	conserved hypothet	histone H1.03 - ch	histone H1.02 - ch	histone H1 - musco	outer membrane ant	tolA protein VC183	histone H1 homolog	histone H1.1 - Cae	histone H1.01 - ch	histone H1-5 [vali	h-caldesmon - chic
T11583	S19113	T06257	B28456	T06636	E75383	D28456	HSCH1	S01262	F71283	A82152	861926	T23778	A23055	S51660	A33430
7	~	~	~	7	N	N	Н	N	N	N	N	0	~	Н	-
1403	265	288	225	924	581	224	218	218	325	356	182	208	218	226	771
32.2	32.1	32.1	31.6	31.6	31.1	31.0	30.7	30.6	30.5	30.5	30.3	30.3	30.3	30.2	30.2
118	117.5	117.5	115.5	115.5	114	113.5	112.5	112	111.5	111.5	111	111	111	110.5	110.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

	7,005,7
	tolA protein - Escherichia coli (strain K-12)
	C;Species: Bscherichia coli
	C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
	R.Levengood, S.K.; Webster, R.E. T. Description 1 171 FEATLEFOR 1 282
	o. parterior. 1.1. (2007-2007) 1.50. and tolk genes and localization of their production.
	A. Reference number: JV0057; MUID:90078104; PMID:2687247
	A; Accession: JV0057
	A; Molecule type: DNA
	A;Residues: 1-421 (LEV>
	A: Experimental source: strain JM105
	A; Note: the authors translated the initiation codon GTG for residue 1 as Val
	R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
	.A.; Rose, D.J.; Mau, B.; Shao, Y.
	Science 277, 1455-1462, 1997.
	A) TITE: III COMPLETE SEGUING SEQUENCE OF ESCRIPTIONS OF A. D.
	A: Accession: B64810
	A; Status: nucleic acid sequence not shown; translation not shown
	A; Molecule type: DNA
	A; Residues: 1-421 < BLAT>
	A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960;
	A, Experimental source: strain K-12, substrain MG1655
	C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach the
	C;Genetics:
	A;Gene: tolA
	A,Map position: 17 min
	A, Start codon: GTG
	C.Keywords: nucleotide binding; P-logy; transmembrane protein
	First 34 Dollarii Cransmeninia factore Arico
	F;78-301/Domain: helical #status predicted <hts>//8-301/Domain: nucleotide-binding motif A (P-loop)</hts>
	Ouery Match 41.1%; Score 150.5; DB 2; Length 421;
	Similarity 53.7%; Pred. No. 0.00023;
-	Qy 3 KYAKKEKAYAKKABKAAKKABAKAYKAABAKKKAKAKABAKKYAKAAKAEKK-EYA 55
	Db 130 KOKQAÉEAAAKAAADAKAKAÉADAKAAEEAAKKAAADAKKKAEAEAAKAAAEAQKKAEAA 189
	Qy 56 aabakykabaakaaakbaayba 77
	100 A11 TUCKET POPULATION 1 11

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19;
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Pred. No. 0.00089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 AAAEAKKKADAAAAKAAADAKKKAAAEKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 AAAEAKYKAEAA-----KAAAKEAA
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44.1%;
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Best Local Similarity 54.4%;
Matches 49; Conservative
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Best Local Similarity 44.1<sup>§</sup>
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Accession: E83525
A; Status: preliminary
A, Molecule type: DNA
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A;Gene: tolA; PA0971
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tolA protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18
C.Species: Salmonella enterica subsp. enterica serovar Typhi
A.Note: this species has also been called Salmonella typhi
C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C.Accession: AGG592
R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q8X965; GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:G
A;Experimental source: strain Ol57:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC80774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane spanning protein TolA [imported] - Escherichia coli (strain 0157:H7, substrain C;5peciese Escherichia coli C;5peciese Escherichia coli C;5peciese Escherichia coli C;5peciese Escherichia coli C;5peciese 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: G85576 Epunkett III, G; Burland, V; Mau, B; Glasner, J.D; Rose, D.J.; Mayhew Iller, L; Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 A;Fitles Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.
A;Reference number: A65480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q8X965; GB:AE005174; NID:g12513672; PIDN:AAG55075.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: tolA
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membrane spanning protein TolA [imported] - Escherichia coli (strain 0157:H7, substrain
             C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: P90725
R;Hayashi, T; Makino, K; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Ogasawara, N.; Yasunaga, T.; Ruhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and Ogasawara, P90725
A;Accession: P90725
A;Accession: P90725
A;Sesidues: 1-394 <HAY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 148; DB 2; Length 394;
Pred. No. 0.00033;
7; Mismatches 21; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.4%; Score 148; DB 2; Length 394;
55.1%; Pred. No. 0.00033;
iive 7; Mismatches 21; Indels 1
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55.1%;
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Matches 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <STO>
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es 49; Conserv
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Asi, Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

Ajuthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

Ajritle: Complete genome sequence of a multiple drug resistant Salmonella enterica serove

Ajritle: Complete genome sequence of a multiple drug resistant Salmonella enterica serove

Ajratus: Complete genome sequence

Ajratus: Moissal

Ajratus: preliminary

Ajmolecule type: DNA

Ajratus: preliminary

Ajmolecule type: DNA

Ajratus: 1-376 <PAR>

Ajratus: Parailass, PIDN:CAD05209.1; PID:g16501979; GSPDB:GN00176

Gjenetics:
Ajratus: Ajratus: Ajratus
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accesino E83525
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A;Reference number: A82950; MUID:20437337; PMID:10984043
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A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  outer membrane integrity protein tolA - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: G64064; JG5212
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A. R;Fleischmann, R.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; MoDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, i. A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; WUID:95350630; PMID:7542800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TolA protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 146; DB 2; Length 37
Pred. No. 0.00044;
7; Mismatches 14; Indels
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R; Knowles, J.A.; Childs, G.J.

Nucleic Acids Res. 14, 8121-8133, 1986
A;Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus and A;Reference number: A25550; MUID:87040778; PMID:3022245
A;Recession: A25550
A;Molecule type: DNA
A;Residues: 1-210 <KNO>
A;Molecule type: UNIPROT:P06144; GB:X04488; NID:99616; PIDN:CAA28177.1; PID:99617
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repetitive protein antigen 27 - Trypanosoma cruzi (fragments)
C;Species: Trypanosoma cruzi
C;Date: 100v-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C;Accession: E60110
R;Hoft, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.; Donelson, J.E.;
Infect. Immun. 57, 1959-1967, 1989
A;Fitle: Trypanosoma cruzi expresses diverse repetitive protein antigens.
A;Fitle: Trypanosoma cruzi expresses diverse repetitive protein antigens.
A;Accession: E60110
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-219 <HOF>
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C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Accession: S5589; 862122
R;Fabry, S; Mueller, K.; Lindauer, A.; Park, P.B.; Cornelius, T.; Schmitt, R.
Curr. Genet. 28, 333-145, 1995
A;Title: The organization structure and regulatory elements of Chlamydomonas histone gene
A;Reference number: S59581; MUID:96120862; PMID:8590479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tandem repeats, each fourteen residues in le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 KTEAQKARAAAKKAKTAAKKKEQKEKKAAKTKARKEKLAAKKAAKKAAKKAYKKPAAKAK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Α.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYA-KAAKAEKKEYAAAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q39576; EMBL:U16726
A;Note: the authors did not translate the codon for residue 1
R;Fabry, S.; Ford, C.; Lindauer, A.; Mueller, K.; Cornelius, T.; Schmitt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
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                                                                                                                                                                                                                                                                                                                                                                Length 210;
                                                                                                                                                                                                                                                                                                                                                             ch 37.2%; Score 136; DB 2; Length 21 Similarity 53.3%; Pred. No. 0.0015; 40; Conservative 7; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.7%; Score 134.5; DB 2; Lengu...
50.7%; Pred. No. 0.002;
Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q26947
C;Comment: This protein contains a series of te
C;Superfamily: neurofilament triplet H protein
C;Keywords: tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S59589
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-231 <FAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 PAKKAAKKPAAKKAA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 TKVAEAGKOKAAEAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 KYKAEAAKAAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 36.7
Best Local Similarity 50.7
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 KYKAEAAKAAAKEAA
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 40; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
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                                                                                       Afforement type: DNA Richard Land Affords (B:U32722; GB:L42023; NID:g1573348; PIDN:AAC22041.1; Risen, K. 5 ikkema, D. 7; Murphy, T.F. Gene 178, 75-81, 1987. Sikema, D. 7; Murphy, T.F. Gene 178, 75-81, 1987. Sikema, D. 7; Murphy, T.F. Gene 178, 75-81, 1987. Sikema, D. 7; Murphy, T.F. A; Reference number: JG5212; MUD:97080550; PMID:8921895 A; Accession: JG5212 MUD:97080550; PMID:8921895 A; A; Aserium ary A; Molecule type: DNA A; A9-141, R', 143-164, P', 166-189, R', 191-202, A', 204-226, A', 228-A; Experimental source: strain 1479 A; Note: the authors translated the codon CGT for residue 190 as Ala C; Genetics: A; Genetics: A; A; Astart codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable erythrocyte-binding protein MAEBL - Plasmodium yoelii C;Species: Plasmodium yoelii C;Species: Plasmodium yoelii C;Species: Plasmodium yoelii C;Date: 11-Jun-1999 #text_change 09-Jul-2004 C;Accession: T09127
R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
A;Title: A family of chimeric erythrocyte binding proteins of malaria parasites. A;Recession: T09127
A;Recession: T09127
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1701 <KAP>
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A; Cross-references: UNIPROT: O61164; EMBL: AF031886; NID: g2947227; PID: g2947228
A; Experimental source: subspecies yoelli; strain YM
C; Genetics:
A; Gene: maebl
A; Introns: 62/1; 1648/1; 1674/2; 1697/1
C; Keywords: alternative splicing; cell binding; erythrocyte invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A25550
histone H1 - sea urchin (Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A25550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKA----EAKKYAKAA-KAEKKEYA---
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Pred. No. 0.0053;
8; Mismatches 16; Indels 13
          A;Accession: G64064
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 38.5%; Score 141; DB 2; Length 372; Best Local Similarity 54.7%; Pred. No. 0.001; Matches 47; Conservative 7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 KAKAAABAKAKADAEAKAATEAKRKA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 KEYAAAEAKYKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1283 KKAEEEKKKAEAAKKAEEE 1301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 54.4%;
Matches 43; Conservative
                                                                         A; Molecule type: DNA
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"TolA colicin import membrane protein [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I.I., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E.
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Drosophila hydei
C;Species: Joil-1996 #squedore_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 351164; S34154
R;Neesen, J.; Padmanabhan, S.; Buenemann, H.
Bur. J. Biochem. 225, 1089-1095, 1994
A;Title: Tandemly arranged repeates of a novel highly charged 16-amino-acid motif represer
lpha-helical rods within the extremely elongated spermatczca of Drosophila hydei.
A;Reference number: S51364; MUID:95045538; PMID:7957199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q8ZGZ2; GB:AL590842; PIDN:CAC89966.1; PID:g15979190; GSPDB:GP
C;Genetics:
                                                                                                                        1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAKA-EKKEYAAAEA
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                                   4; Gaps
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A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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                                      Indels
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51.4%; Pred. No. 0.0061;
Micmatches 20;
        Local Similarity 52.7%; Pred. No. 0.0035; hes 39; Conservative 9; Mismatches 22;
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A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1390 <NES>
A;Cross-references: UNIPROT:Q08696; EMBL:X73481
R;Neesen, J.; Heinlein, U.A.O.; Buenemann, H. submitted to the EMBL Data Library, June 1993
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                                                                                                                                                                                                                                                               167 TKVAEAEKOKAAEA 180
                                                                                                                                                                                                          60 KYKAEAAKAAAKEA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 51.4%
Matches 37; Conservative
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214 VEVAEKAAADAA 225
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A; Accession: S34154
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           Best Loc
Matches
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A;Description: The organization, structure and controlling elements of Chlamydomonas his A;Reference number: S62122
A;Reference number: S62122
A;Rolecule type: DNA
A;Rossidue: 1-173, 'P', 174-231 <FAW>
A;Cross-references: EMBL:U16726; NID:g571479; PIDN:AAA98452.1; PID:g571480
C;Genetics: C3,3; 101/3
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: DNA
A,Residues: 1-1128 <OTS>
A,Cross-references: UNIPROT:Q26947; EMBL:L04603; NID:g385171; PID:g1256742; PIDN:AAA9649
C,Superfamily: neurofilament triplet H protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytobolic repetitive antigen - Trypanosoma cruzi (fragment)
C;Species: Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A44993
R;Lafaille, J.J.; Linss, J.; Krieger, M.A.; Souto-Padron, T.; de Souza, W.; Goldenberg, A)C. Biochem. Parasitol. 35, 127-136, 1989
A;Title: Structure and expression of two Trypanosoma cruzi genes encoding antigenic prot A;Reference number: A44993; MUID:89364992; PMID:2475776
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                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 36.6%; Score 134; DB 2; Length 1128; Best Local Similarity 52.0%; Pred. No. 0.0076; Matches 39; Conservative 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.3%; Score 133; DB 2; Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A44993
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-328 <LAF>
                                                                                                                                                                                                                                                                                                                                                  Score 134.5; DB 2; Length 2 Pred. No. 0.0021; 4; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 KPKAAKPAKKTTKKAAAKPKAEKKPKAAAKPKA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 KEYAA-----AEAKYKAE-AAKAAKEAA 74
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C;Superfamily: neurofilament triplet H protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1032 TKVAEAEKQKAAEAA 1046
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Grobable hupB - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: G70673
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Majuthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Sarrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MuID:98295987; PMID:9634230
A;Reference number: A70500; MuID:98295987; PMID:9634230
A;Recession: G70673
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-214 cCOL>
A;Cross-references: UNIPROT:P95109; GB:Z83018; GB:AL123456; NID:g3261671; PIDN:CAB05427.
C;Genetics:
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                                                                                                  2 KKYAKKEK--AYAKKAEKAAKK----AEAKAYKAAEAKKKAKAEAKKYAKAAK----AE 50
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   1 Similarity 51.7%; Pred. No. 0.018;
45; Conservative 3; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 TKAVKKTAVKASVRKAATKAPAKKAAAKRPATKA 202
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Best Local Similarity
Matches 45; Conserv
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Enterobacteriaceae; Shigella.
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Q8mi6 pseudomonas
Q6d7f3 erwinia car
P50600 pseudomonas
P4678 haemophilus
Q9cm70 pasteurella
Q6miu4 bdellovibri
Q7n6t7 photorhabdu
Q39576 chlamydomon
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Aaq73455 plasmodiu
Aaq33457 plasmodiu
061164 plasmodium
P06144 lytechinus
Q6cdx0 yarrowia li
Q98kg7 rhizobium li
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erwinia chr
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Aaq73456 plasmodiu
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                                                                                          December 14, 2004, 05:47:53 ; Search time 86.4219 Seconds (without alignments) 512.646 Million cell updates/sec
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770LA 77

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98X976

98X971

98X971

997RC08

99WX1

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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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Q6n503 rhodopseudo
Cae28621 rhodopseu
Q87y39 pseudomonas
Q6F986 acinetobact
Q6n8x8 rhodopseudo
Cae27215 rhodopseu
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Q8czz8 yersinia pe
Q08696 drosophila
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                  Aar37978 unculture
Q26947 trypanosoma
                                                      yersinia pe
                                                   Q74w64 yersinia pe
Aas61283 yersinia
   uncultured
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAYAKKAEKAKKAEAKAYKAAEAKKKAKAKAEAKKYAK-----AAKAEKK-E
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EMBL; AB016979; AAP16075.1; -. EMBL; AB016979; AAP16075.1; -. Flacency PF06519; TollA: TollA: TollA: SEQUENCE 413 AA; 42355 MW; 93E10F2C5DE60DE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q83SA1;
Q913SA1;
Q913CA1;
Q913CA1;
Q91-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 26, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Membrane spanning protein, required for outer membrane integrity.
Name-tola, OrderedLocusNames=SF0558;
Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.7%; Score 152.5; DB 2; Length 413; 52.4%; Pred. No. 0.00077; ive 11; Mismatches 22; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         413 AA
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                                                   Q74W64
AAS61283
Q6N503
CAE28621
 Q6SG84
AAR37978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Membrane spanning protein.
Name=tolA, OrderedLocusNames=80571;
Shigella flexneri.
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Q6F986
Q6N8X8
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Q8CZZ8
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Best Local Similarity 52.4<sup>†</sup>
Matches 44; Conservative
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NCBI_TaxID=623;
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'TolA central domain interacts with Escherichia coli porins.";
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TOLA_ECOLI
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MEDLINE-22827954; PubMed=12910271; DOI=10.1038/ng1227;

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Cardeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

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Leather S., Moule S., Norberczak H., Holroyd S., Jagels K.,

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Rabbinowisceh E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Salchon J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

Comparative analysis of the genome sequences of Bordetella pertussis,

Bradetella parapertussis and Bordetella bronchiseptica.";

Nat. Genet. 35:32-40(2003).

Rembi. Bacdetella parapertussis and Bordetella bronchiseptica.";

GO; GO:0010203; C:membrane; IEA.

GO; GO:0010203; P:protein transporter activity; IEA.

InterPro; IRR00528; Toll.

Rem Harch Pro; Toll Pro; Toll Pro; Toll Pro; Toll Pro; Toll Pro; Tol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAK-----AAKAEKK-E 53
                                                      STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin O., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                     "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157."i, Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                   7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                        ch 41.7%; Score 152.5; DB 2; Length 413; I Similarity 52.4%; Pred. No. 0.00077; 44; Conservative 11; Mismatches 22; Indels 7;
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01-MAR-2004 (TrEMBLrel. 26, Last anno
Proline-rich inner membrane protein.
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TIGRFAMB; TIGR01352; tonB_Cterm; 1.
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                                                                                                                                                                                                                                             EMBL; AE015086; AAN42202.1; -. HSSP; P19934; 1TOL.
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NCBI_TaxID=518;
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STRAIN=RBS0 / ATCC BAA-588;
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Best Local Similarity
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                                     FROM N.A.
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 NCBI_TaxID=623;
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01-MAR-2004
                                     SEQUENCE
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Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Santo M.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.C., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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J. Bacteriol. 171:6600-6609(1989).
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Enterobacteriaceae, Escherichia.
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Levengood S.K., Beyer W.F. Jr., Webster R.E.;
"TolA: a membrane protein involved in colicin uptake contains an
extended helical region.";
Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943(1991).
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                                                                                                                                        Length 379;
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379 AA; 40776 MW; C657B5AAE97EBDD3 CRC64;
                                                                                                                   Query Match 41.3%; Score 151; DB 2; Best Local Similarity 57.0%; Pred. No. 0.00093; Matches 45; Conservative 8; Mismatches 20
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01-FEB-1991 (Rel. 17, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
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STRAIN=K12 / JM105;
MEDLINE=90078104; PubMed=2687247;
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MEDLINE=97061202; PubMed=8905232;
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NCBI_TaxID=519;
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Q7AGI8,
05-JUL-2004 (
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                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                     Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.,
Lubkowski J., Hennecke F.,
"Filamentous phage infection: crystal structure of g3p in complex with
its corceptor, the C-terminal domain of TolA.";
Structure 7:711-722(1999).
-!- FUNCTION: Involved in the tonB-independent uptake of group A
colicins (colicins A, B1, E2, B3, and K). Necessary for the
colicins to reach their respective targets after initial binding
to the bacteria. Also involved in the translocation of
                                                                                                                                                                                                                                                                                                                                                                                                                    Periplasmic (Potential).

DOMAIN II (ALPHA-HELICAL).

DOMAIN III (FUNCTIONL).

13 tandem repeats of [EDA]-K(1,2)-A(2,4).
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1 13 Cytoplasmic (Potential).
RRANSMEM 14 34 Potential.
                                                                                                                                                              SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                              bacteriophage DNA. SUBUNIT: Interacts, via domain II, with porins ompC, phoE and
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                                                                                                                                                                                                                                                                                                                                                                          Bacteriocin transport; Complete proteome;
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                   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421.
MEDLINE=99332679; PubMed=10404600;
                                                                                                                                                                                                                                                                         EMBL; M28232; AAA24683.1; -.
EMBL; AE00017; AAC73833.1; -.
EMBL; D90713; BAA35405.1; -.
PIR; JV0057; JV0057.
EDB; HTCL; X-ray; A=-.
ECHORASE; EB1000; -.
ECGGEDE; EG11007; ColA.
EMBO J. 15:6408-6415(1996).
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Pfam; PF06519; TolA; 1.
3D-structure; Bacteriocin t
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Gaps

7;

Best Local Similarity 53.7 Matches 44; Conservative

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SEQUENCE FROM N.A.

STRAIN=12822 / ATCC BAA-587;

STRAIN=12822 / ATCC BAA-587;

MEDLINE=22827954;

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Cardeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

A Chillingworth T., Collins M., Cronin A., Davis B., Doggett J.,

A Chillingworth T., Collins M., Cronin A., Davis B., Doggett J.,

A Rebinowits B., Norberczak H., O'Neil S., Ormond D., Price C.,

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"Comparative analysis of the genome sequences of Bordetella pertussis,

I'm Bordetella parapertussis and Bordetella bronchiseptica.";

Nat. Genet. 35:32-40(2003).
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KYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAK-----AAKAEKK-EYA
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Membrane spanning protein TolA.
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                                                                                                                                                                               190 AAALKKKAEAAEAAAEARKKA 211
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239 KAKEEAAKKAAADKA 253
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Bordetella parapertussis.
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Q7AGI8
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138 AAKAAADAKAKAEADDKAAEEAAKKAAADAKKKAEAEAAKAAAEAQKKAEAAAALKKKA 197
407 AA
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                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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MEDLINE-21534948; PubMed=11677609;
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NCBI_TaxID=217992;
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InterPro; IPR010528; TolA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TolA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                  Q8ZQT6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBFJT1
                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
                                                                                                                                                                                                                                                                                      QBZQT6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBFJT
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                                                                                                                                                                                                            MEDLINE=21156231; PubMed=11258796; MEDLINE=21156231; PubMed=11258796; MEDLINE=21156231; PubMed=11258796; MEDLINE=21156231; PubMed=11258796; MEDLINE=21156231; PubMed=11258796; Midna=2.1. Shakino K., Vohcyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=0157.H7 / EDL933 / ATCC 700927 / EHEC;
STRAIN=0157.H7 / EDL933 / ATCC 700927 / EHEC;
STRAIN=01074935; PubMed=11206531,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Fosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Membrane spanning protein, required for outer membrane integrity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.4%; Score 148; DB 2; Length 394; 55.1%; Pred. No. 0.0016; ive 7; Mismatches 21; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40517 MW; 5B58D8E8230BDE28 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP002553; BAB34197.1; -. InterPro; IPR010528; TolA.
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EMBL; AR005252; AAGS5075.1; -.
PIR; P90725; P90725
PIR; G85576;
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49; Conservative
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      OrderedLocusNames=ECs0774;
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Pfam; PF06519; Tola; 1.
                                         Escherichia coli 0157:H7.
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                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                               NCBI_TaxID=83334;
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01-MAR-2002
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RESULT 7 Q8X965

Matches

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Atterston R., Wilson R.K.;" (Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388234; PubMed=12471157; Welfor R.A., Burlan V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.P., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                        Tol protein, membrane spanning protein.
Mame=tolk) OrderedLocusNames=STM0747;
Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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40.4%; Score 148; DB 2; Length 40
Best Local Similarity 54.4%; Pred. No. 0.0016;
Matches 49; Conservative 8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407 AA; 41865 MW; 2534352116602D75 CRC64;
Last sequence update)
Last annotation update)
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(TrEMBLrel. 26, Last annotation update)
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182 AKKKAEEEAKTKAAAAAEAKKKAEEEAKAKAAAADAKQKAEEEAK--AKAAA-AKEKAAA 238
                               1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-AAEAKKKAKAEAKKYAKAAKAEKK-----EY 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.8%; Score 145.5; DB 2; Length 395; 61.0%; Pred. No. 0.0024; ive 9; Mismatches 14; Indels 7
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ray M.C., Vianney A., Cotte-pattat N., Lazzaroni J.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ297885; CAC62708.1; -.
HSSP; P19934, ITOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO10528; TolA.
Pfam; PF06519; TolA; 1.
SEQUENCE 395 AA; 41601 MW; 3COCIDC12E181013 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Brythrocyte binding protein.
                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                        55 AAAEAKYKAEAA-----KAAAKEAA
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Best Local Similarity 61.0°
Matches 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erwinia chrysanthemi.
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NCBI_TaxID=73239;
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                                                                                                                                                                                                                                                                                                                                                                                                               Tola protein.
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Q937K4;
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Q7RC08;
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STRARIE-TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=2154947; PubMed=11677608; DOI=10.1038/35101607;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella
enterica servora Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                     3 KYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKK--YAKAAKA-----EKKEYA
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
EMBL; AR016757; AAN79291.1; -.
HSSP; P19934; 1170L.
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                            ch 40.3%; Score 147.5; DB 2; Length 421; 1 Similarity 53.7%; Pred. No. 0.0018; 44; Conservative 7; Mismatches 24; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 39.9%; Score 146; DB 2; Length 376; Best Local Similarity 54.4%; Pred. No. 0.0022; Matches 49; Conservative 7; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            376 AA; 38804 MW; EC21F2C4767A8A42 CRC64;
                                                                                                                                                                                                                                421 AA; 43184 MW; DB296626F056D385 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q828C1; Q7C8P3;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=tolA; OrderedLocusNames=STY0793, t2129;
Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 AAALKKKAEAAEAARKKA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
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EMBL, AL627268; CAD05209.1; --
EMBL, AE016841; AA069743.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 AAEAKYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P19934; ITOL.
InterPro; IPR010528; TolA.
Pfam; PF06519; TolA; 1.
Complete proteome.
SEQUENCE 376 AA; 38804 MA
                                                                                                                                                    InterPro; IPR010528; TolA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                         Pfam; PF06519; TolA; 1.
Complete proteome.
SEQUENCE 421 AA; 4316
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Best Local Similarity
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GO:0006334; P:nucleosome assembly; IEA.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=160488;
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Q88NI6
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                                                                                                                                                                            1 AKKYAKKEKA-YAKKAEKAAKKAEAKAYKAAEAKKKAKA----EAKKYAKAKA--AEK
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.; "The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96422022; PubMed=8824639;
Rodriguez-Herva J.J., Ramos J.;
"Characterization of an OprL null mutant of Pseudomonas putida.";
J. Bacteriol. 178:5836-5840(1996).
        Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                  Query Match
39.1%; Score 143; DB 2; Length 1701;
Best Local Similarity 55.3%; Pred. No. 0.012;
Matches 47; Conservative 7; Mismatches 17; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0016020; C:membrane; IEA.
GO; GO:0000786; C:nucleosome; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0008565; F:protein transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                               STRAIN=mt-2;
Ramos-Gonzalez I.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                            372 AA
                                                                                                                                                                                                                                        1329 KKAEAAKKAEEEKKKAEAAKKAEEE 1353
                                                                                                                                                                                                                    52 KEYAAA----EAKYKAEAAKAAAKE 72
parasite Plasmodium yoelii yoelii.";
                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=303;
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Submitted (UTL-1999) to the E
EMBL; X74218; CAB50780.1; -.
HSSP; P50600; LIRO.
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                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas putida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 envelope.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKA------YAKKAEKAAKKA---EAKAYKAAEAKKKAKAEAKKYA--- 44
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GO; GO:0000786; C:nucleosome; IEA.
GO; GO:00005634; C:nucleos; IEA.
GO; GO:00005634; C:nucleos; IEA.
GO; GO:00005634; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0008565; F:protein transporter activity; IEA.
GO; GO:0005331; P:nucleosome assembly; IEA.
InterPro; IPR005819; Histone H5.
InterPro; IPR010528; TolA.
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                                                                                                                                                                                                                                                                                                                                                                                                                  21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 372;
                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ Microbiol. 4:799-808 (2002). EMBL; ARO16778, AANG6845.1; -. HSSP; P50600; 1LR0.
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                            Pfam; PF06519; TolA; 1.
PRINTS; PR00624; HISTONEH5.
TIGRFAMs; TIGR01352; tonB Cterm; 1.
SEGUENCE 372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUNAR-2004 (TrEMBLrel. 26, Last annotation update)
Biopolymer transport protein TolA.
Name=tolA, OrderedLocusNames=PP1221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 ---KAAKAEKKEYAAAEAKYK--AEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                           38.9%; Score 142.5; DB 2;
46.9%; Pred. No. 0.0039;
iive 10; Mismatches 21;
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GO; GO:0006334; P:nucleosome assembly; IE. GO; GO:0015031; P:protein transport; IEA. InterPro; IPR0105819; Histone_H5. InterPro; IPR010528; TolA. InterPro; IPR06260; TonB_C.
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TIGRFAMs; TIGR01352; LonB_Cterm; 1.
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Best Local Similarity 46.9%
Matches 46; Conservative
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A [1]

REGUENCE FROM N.A.

SEQUENCE FROM N.A.

RA STRAIN=SCRIIO143;

RA HOLeva M.C., Thomson N.R., Bentley S.D., Churcher C., Mungall K.,

RA ARkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,

RA Arkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,

RA Arkin R., Bason N., Brooks K., Chillingworth T., Clark K.,

RA Arkin R., Bason N., Brooks K., Chillingworth T., Clark K.,

RA Arkin R., Bason N., Brooks K., Chillingworth T., Clark K.,

RA Arkin R., Bason N., Brooks K., Chillingworth T., Clark K.,

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RA Arkin R., Bason N., Brooks K., Chillingworth T., Chark K.,

RA Arkin R., Bason N., Brooks K., Chillingworth T., Chil
                                                                                                                                                                                        5 AKKEKAYAKKAEKAAKKAEAKAYK----AAEAKKKAKAEAKKYAKAAKA-----EKKE 53
                                                                                                                    1 AKKYAKKEKA----YAKKAEKAAKKA--EAKAYKAAEAKKKAKAEAKKYA--- 44
      21; Gaps
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Name=tola; ORFNames=ECA1372;

Barunia carotovova subsp. atroseptica SCRII043.

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae, Pectobacterium.
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      21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            208 AKKKAAAEDAKKKAAEEAKKKAAADAQKKKAQEAARKA 245
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01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                        45 ---KAAKAEKKEYAAAEAKYK--AEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395 AA
      10; Mismatches
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      46; Conservative
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Best Local Similarity
Matches 46; Conserv
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194 KAAEAAKQKAAETAKAEAAKAAA-EAAKEA 222

Search completed: December 14, 2004, 06:10:18 Job time : 86.4219 secs

54 YAAAEAKY----KAEAAKAAAKEAAYEA 77

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Compugen Ltd.
version 5
GenCore (c) 1993
       Copyright
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- protein search, using sw model OM protein

December 14, 2004, 05:47:53 ; Search time 85.1224 Seconds (without alignments) 324.499 Million cell updates/sec Run on:

US-10-792-311-5 366 Perfect score:

77

1 AKKYAKKEKAYAKKAEKAAK.......EAKYKAEAAKAAAKEAAYEA Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:* A Geneseq 23Sep04:* geneseqp1980s:* geneseqp1990s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

1 ID Description	AAY82575 Aay82575 Copolymer	_	_	_	_		ABU47123 Abu47123 Protein	ABU44721 Abu44721 Protein	Abu47848	AAY98499 Aay98499 Peptide	AAY59044 Amino aci	AAB45852 Aucleic	AAU04289 Aau04289 Poly-Lys	ABU27824 Abu27824 Protein	: AAR06445 Recombina	ABU40185 Abu40185 Protein	; ABU31397 Abu31397 Protein	ABU38313 Abu38313 Protein	ABJ18771 Pseudomon	/ ABO80835	, ABO67048 Abo67048 Klebsiel	ABG80418 Abg80418 Haemophi	, ABO23507 Haemophi	AARO6446 Recombina
DB		m	m	٣	m	9	9	9	9	٣	m	4	4	9	7	9	9	9	9	7	7	Ŋ	7	c
Length	77	86	109	99	56	421	407	387	376	100	100	100	100	428	154	372	323	347	347	407	469	372	372	106
% Query Match	100.0	96.0	79.0	77.2	67.1	41.1	40.4	40.0	39.9	39.5	39.5	39.5	39.5	39.3	38.9	38.9	38.7	38.7	38.7	38.7	38.7	38.5	38.5	38.3
Score	366	351.5	289	282.5	245.5	150.5	148	146.5	146	144.5	144.5	144.5	144.5	144	142.5	142.5	141.5	141.5	141.5	141.5	141.5	141	141	140
Result No.	1	7	ო	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

m F F F	_			Ada33882 Acinetoba Abg71044 Tumour ne Ada35034 Acinetoba Abp57088 Mouse MKP Abu33811 Protein e
ABM67869 AAR84568 ADQ36692	ADQ366/8 ABU42038 AAY82572 ABU50266	AAR84569 AAR84569 AAR84565 AAY34055	AAY57353 ABU34623 ABU36893 ADF05105	ADA33882 ABG71044 ADA35034 ABP57088 ABU33811
9789	იდოდი	2000	7007	စစစစစ
357 643 507	336 336 388 388	205 472 564 214	214 214 214 361	214 80 468 452 212
37.8 36.6 36.1	35.9 35.9 35.7	2.25.25 2.25.25 2.25.4.	35.4 35.4 35.4	35.1 34.7 34.3 33.9
138.5 134 132	131.5 131.5 131	130 130 130 129.5	129.5 129.5 129.5 129.5	128.5 127 125.5 124.5 124
24 27 28	33333	2 2 2 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	3 3 3 4 4 0 4	4 4 4 4 1 2 6 4 6 1 5 6 7 9

ALIGNMENTS

glatifamer acctate, autoimmune disease, antiarthritic; neuroprotective, osteopathic; immunosuppressive, antithyroid, antiinflammatory; antidabetic; thyrominetic; haemostatic; antibaoriatic; dermatory; antidabetic; thyrominetic; haemostatic; antibaoriatic; dermatory; antianaemic; immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopachic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5. Copolymer; molecular weight marker; TV-marker; immune disease; AAY82575 standard; peptide; 77 AA. (first entry) 28-JUL-2000 AAY82575;

Unidentified,

WO200018794-A1.

06-APR-2000.

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; Gad A, WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

Claim 10; Page 14; 72pp; English.

```
of the invention are used as molecular weight markers for glatiramer acctate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases. Such diseases include arthritic conditions, demyelinating arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune chyroiditis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, draves disease, diillain-Barre's syndrome, Hashimoto's disease, idiopathic mycoedema, myasthenia gravis, peoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The popperties which are analogous too glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
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Sequence 77 AA;

9 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK Gaps ; 0 Length 77; 0; Indels 100.0%; Score 366; DB 3; 100.0%; Pred. No. 7.3e-27; ive 0; Mismatches 0; YKAEAAKAAAKEAAYEA 77 61 YKAEAAKAAAKEAAYEA 77 61 ద ò 9 ò

AAY82576 standard; peptide; 86 AA.

(first entry) 28-JUL-2000

AAY82576;

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.

antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; osteopathic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; Hashimoto's disease, idiopathic myxoedema, myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified

WO200018794-A1

06-APR-2000.

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD (TEVA-) TEVA PHARM USA INC. (YEDA) YEDA RES &

Lis D; Gad A, WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

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diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune harmolytic anaemia, autoimmune dopontritis, autoimmune thyroiditis, autoimmune uporetrinitis, contact disease, chronic immune thrombocytopeania purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto, 6 disease, idiopathic myxoedema, mysathenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host versus-graft disease, graft versus-nost disease, and delayde-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which
                                                                                                  weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatinamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include atther cell mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                             AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.0%; Score 351.5; DB 3; Length 86; 89.5%; Pred. No. 1.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                properties which are analogous to glatiramer acetate makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 89.5<sup>3</sup>
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 86 AA;
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYAABAKKKAKAEAKKYAKAAKAEKKEYAAAEAK

1 AKKYAKKEKAYAKKAEKBAKKAEAKAYKAABAKKKAKAEKKAYAKAEKKBYAAAEAK 86 77 61 -----YKAEAAKAAAKEAAYEA 셤 ð 셤

9

AAY82577 standard; peptide; 109 AA AAY82577;

AAY82577

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.

glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyrominetic; haemostatic; antibaoriatic; dermatory; antidabetic; immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer; molecular weight marker; TV-marker; immune disease;

Unidentified.

40200018794-A1.

06-APR-2000.

99WO-US022402 24-SEP-1999;

98US-0101693P. 25-SEP-1998;

(YEDA) YEDA RES & DEV CO LTD

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AAY92571 to AAV82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glattramer actated retrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a maimmal. Autoimmune diseases of treating and preventing immune diseases in a maimmal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, contact disease, chronic immune thyroidmine haemolytic anaemia, autoimmune thyroidmine the composition of disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashinoto's disease, idiopathic mysocedema, mysathenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythemacosus. Mediated mediated diseases which can be treated include host-versus-graff disease, propperties which are analogous to glatiramer accetate molecules, which compared the markers molecular weight markers
                                                                                                                                                                 Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                                                                                                              Claim 10; Page 14; 72pp; English.
(TEVA-) TEVA PHARM USA INC
                                                                                                           WPI; 2000-317499/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 109 AA;
                                                        Lis D;
                                                     Gad A,
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36 Gaps 32; 61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109 37 -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA 77 79.0%; Score 289; DB 3; Length 109; 67.0%; Pred. No. 1.5e-19; ive 1; Mismatches 3; Indels 1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKA----Local Similarity 67.0 Les 73; Conservative Query Match fatches Š 셤 ⋧ 셤

AAY82574 standard; peptide; 66 AA. AAY82574; RESULT 4

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; ornonic immune thrombocytopaenia purpura; colitis; diabetes mellitus; draves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified

WO200018794-A1

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer accetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating cophoritis, autoimmune thyroidmins, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune thyroidmins, e.g. multiple sclerosis, crontact cophoritis, autoimmune thyroidmins, e.g. multiple sclerosis, crontact arthritis, osteoarthritis, autoimmune thyroidmins, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxacedema, myashiming gravis, contact compliated disease, which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The copyractics which are analogous to glatiramer accetate molecules, which completed properties which are analogous to glatiramer accetate molecules, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antiannemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                             Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.2%; Score 282.5; DB 3 84.4%; Pred. No. 3.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY82573 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 14; 72pp; English.
                                                                                                                                           (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
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                                                             99WO-US022402.
                                                                                                    98US-0101693P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 YKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                    WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 66 AA;
                                                             24-SEP-1999;
                                                                                                      25-SEP-1998;
                 06-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY82573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                             Gad A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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9 49 Antisense; prokaryotic essential gene; cell proliferation; drug design.

Escherichia coli

WO200277183-A2 03-OCT-2002

Protein encoded by Prokaryotic essential gene #14086.

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syndrome; psoriasis;
                                                                                                                                                                                              Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
Crohn's disease; chronic immune thrombocytopaenia purpura; colitis;
       diabetes mellitus, Graves disease, Guillain-Barre's syndrome,
Hashimoto's disease, idiopathic myxoedema, myasthenia gravis,
pemphigus vulgaris, systemic lupus erythematosus.
                                                                                                                                                                                                                        Claim 10; Page 14; 72pp; English.
                                                                                                                                 DEV CO LTD.
USA INC.
                                                                                                99WO-US022402.
                                                                                                               98US-0101693P.
                                                                                                                                                                             WPI; 2000-317499/27
                                                                                                                                (YEDA ) YEDA RES & (TEVA-) TEVA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 56 AA;
                                                            WO200018794-A1
                                                                                                                                                            Gad A, Lis D;
                                          Unidentified
                                                                                                24-SEP-1999;
                                                                                                                25-SEP-1998;
                                                                              06-APR-2000
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screening

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New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD,

'nά Wang Wall WPI; 2003-029926/02. N-PSDB; ACA32429.

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0192923P. 08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P. (ELIT-) ELITRA PHARM INC.

21-MAR-2002; 2002WO-US009107

The invention relates to an isolated nucleic acid comprising any one of

Claim 25; SEQ ID NO 56483; 1766pp; English.

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides [1] for determining the molecular weight to invention describes polypeptides [1] for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer accetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, eg. multiple sclerosis, rheumatory conditions, eg. multiple sclerosis, rheumatory conditions, eg. multiple sclerosis, cronn's disease, chronic immune thyroidmine haemolytic anaemia, autoimmune cophoritis, autoimmune thyroidmine, graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic mysoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, physperides of the invention have defined molecular weights and physical properties which are analogous to glatiramer accetate molecules, which makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 245.5; DB 3 Pred. No. 7.7e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.1%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 72.7
Matches 56; Conservative
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the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

comprising a promoter operably linked to the nucleic acid

concomprising a promoter operably linked to the nucleic acid

concoding a polypeptide whose expression is inhibited by the antisense

concleic acid; (2) a host cell containing the vector; (3) an isolated

concleic acid; (2) a host cell containing the vector; (3) an isolated

contisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide or the activity of a gene in an operon required for

contisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide or the activity of a gene in an operon required for

proliferation or the activity of a gene in an operon required for

contisense or the activity of a gene in an operon required for

proliferation or that has an activity against a biological pathway to the proliferation or that inhibits cellular proliferation; (8)

confentifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprise or collection of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational correlations or screening for homologous nucleic acids required for proliferation are sereening for homologous nucleic acids required for proliferation and isolate candidate modeled accids when the required for proliferation is a present accompound that inhibits the required for proliferation is a present accompound and accided the

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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK
                          ----AEAK
                        1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK---
                                                                                                                                     ABU28559 standard; protein; 421 AA.
                                                61 YKAEAAKAAAKEAAYEA 77
                                                             RESULT 6
ABU28559
ID ABU2
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AC ABU2
XX
DT 19-J
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                                                ò
ò
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(first entry)

19-JUN-2003

ABU28559;

39

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3 KYAKKEKAYAKKAEKAAKKAEAKAYKAEAKKKAKAEAKKYAK-----AAKAEKK-EYA
                        7; Gaps
                        Indels
Score 150.5; DB 6
Pred. No. 4.3e-06;
8; Mismatches 23
 41.1%;
53.7%;
                          44; Conservative
 Query Match
Best Local Similarity
                          Matches
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K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

ζ,

DB 6;

Sequence 421 AA;

55

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the invention fraction to an instance and compitating any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense ancient acid; (2) a host cell containing the vector; (3) an isolated canding appropriate whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway consideration; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway consideration or that has an activity against a biological pathway or the proliferation or that inhibits cellular proliferation; (8) centured for proliferation or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of the strains is present in a culture or collection of compound; activity; (11) a culture compound that inhibits or strains; or (13) identifying the target of a compound that inhibits the extent of strains; or (13) identifying the target of a compound that inhibits or collection of compound that inhibits or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening them of an organism. The present sequence is encoded by one of conditive drug discovery programs, or for screening themselvents is an encoded by one of conditions or p. aeruginosa. The present sequence is encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
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Yamamoto R, Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #32650.
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                                                                                                                                                                                                                                              ABU47123 standard; protein; 407
56 AAEAKYKAEAAKAAAKEAAYEA
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Carr GJ,
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25-0CT-2001; 2001US-0342923P.
08-FEBS-2002; 2002US-00072851
06-MAR-2002; 2002US-0362699P.
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Trawick JD,
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Wall
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ABU47123

ID AH123

ID AH123

ID AH123

ID AH17123

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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8)
                                                                                                                                                                                                             screening
the target prokaryotic essential genes. Note: The sequence data for this spatent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fto, wipo.int/pub/published_pct_sequences
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Xu HH;
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for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                     20;
                                                                                                                     Length 407;
                                                                                                                   40.4%; Score 148; DB 6; Length 40 larity 54.4%; Pred. No. 7e-06; Conservative 8; Mismatches 13; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #30248.
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Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                                                  ABU44721 standard; protein; 387 AA
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Carr GJ,
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-0372851.
06-MAR-2002; 2002US-0362699P.
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Trawick JD,
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                                                                                                                               Local Similarity
ses 49; Conserv
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                                                                                    Sequence 407
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Wall D,
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identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the strains; or (13) identifying for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational for cellular proliferation in calls other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained to the control of the printed specification, but was obtained to the control of the printed specification, but was obtained to the control of the printed specification, but was obtained to the control of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                        40.0%; Score 146.5; DB 6; Length 387;
58.6%; Pred. No. 9.2e-06;
.ive 7; Mismatches 16; Indels 13; Gaps
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Xu HH;
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Yamamoto R, Forsyth RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 AAEAKYK--AEAAKAAA---KEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU47848 standard; protein; 376 AA.
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06-MAR-2002; 2002US-0362699P
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Trawick JD,
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N-PSDB; ACA51718.
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 387 AA;
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Wall D,
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ABU47848
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Claim 25; SEQ ID NO 75772; 1766pp; English.

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the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a product operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated of nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for che gene product or that has an activity against a biological pathway required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product is overexpressed for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or organism. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids are useful for confileration of an organism. The antisense nucleic acids are called for proliferation in cells other than S, aureus, S, typhimurium, CC for cellular proliferation in cells other than S, aureus, S, typhimurium, CC the target prokaryotic essential genes. Note: The sequence is encoded by one of the target processor of the particular proliferation of the particular proliferation of the particular proliferation of the p
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                 The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression
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Pred. No. 9.9e-06;
7; Mismatches 14; Indels 2
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93WO-US002725.
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il Similarity 54.4%;
49; Conservative
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Best Local Similarity
Matches 49; Conserv
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19-MAR-1993;
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    PAR Y 
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                                                                                                                                                                                                                                                     The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36633-A36652 and peptide sequences AAA36633-A36650 are used in gene therapy, particularly to deliver creating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transgenic animals (as models for human carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro corrections function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from endosomes, without requiring endosomal or lysosomal degradation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3. .100 //note= "Lys-Ala in positions 3 to 100 may be optionally absent"
                                                                                                               System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid transport system; NTS; cell surface receptor; cytosis; nuclear membrane; lysis moiety; transgenic animal; human disease; nucleic acid delivery; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.5%; Score 144.5; DB 3; Length 100; 58.4%; Pred. No. 3.3e-06; ive 6; Mismatches 23; Indels 3
                        Smith LC;
                           WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid polymer seq ID NO: 64 of US5994109.
                                                                                                                                                                                                                  Disclosure, Col 125-128, 108pp, English.
                        Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY59044 standard; peptide; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 AKAKAKAKAKAKAKA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00460890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 AKYKAEA-AKAAAKEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 58.4
nes 45; Conservative
                        Sparrow J,
                                                                  WPI; 2000-281993/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                        Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY59044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
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The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or artigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moving or initiating movement through a nuclear membrane; and/or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytoplasm of the cell. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting specific nucleic acid accordingly. The NTS can also be used to oreate transgenic animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells. The NTS can be used in vitro with tissue culture cells. The yest agent within the NTS avoids the problem of endosomal/lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۳
ښ
                                                                                                                                                                                                                                                     Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.5%; Score 144.5; DB 3; Length 100; 58.4%; Pred. No. 3.3e-06;
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                                                                                                                            Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                            Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.4%; Pred. No. 11.
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 123-124; 107pp; English
                                                                                                                            Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB45852 standard; protein; 100 AA.
                                                            (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74
93US-00167641.
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62 AKAKAKAKAKAKAKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45; Conservative
                                                                                                                            Cristiano RJ,
                                                                                                                                                                                         WPI; 2000-038262/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacterial antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jnidentified
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14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6150168-A.
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The sequence represents poly-Lys-Ala, used to bind nucleic acid in a nucleic acid transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules, lysis agents and spacer molecules are used in nucleic acid transporter systems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells
                                                                                                  nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #13351
                                                                                                                                                                                                                                                                                                                                                                                 39.5%; Score 144.5; DB 4; 58.4%; Pred. No. 3.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                          Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ď,
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
                                                                                                                                                 Disclosure, Col 131; 111pp; English.
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                                          Cristiano RJ,
              (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU27824 standard; protein; 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 AKYKAEA-AKAAKEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 58.4
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003-029926/02
                                            Smith LC,
                                                                        WPI; 2001-365933/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-029926/
N-PSDB; ACA31694.
                                                                                                                                                                                                                                                                                                                                                    Sequence 100 AA;
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Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
ABU27824
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ठे
                                                                                                                                                                                         This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid. The nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor applications with antigens, parasitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid transport; cytosis; ligand; lysis agent; spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3. .100
/note= "Lys-Ala in positions 3-100 may be present or
                                                                                                   Nucleic acid transporter system for delivering nucleic acid into a ouseful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 100;
                                            WOO SLC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poly-Lys-Ala used in nucleic acid transporter system.
                                          Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 144.5; DB 4
Pred. No. 3.3e-06;
6; Mismatches 23
                                            Cristiano RJ,
                                                                                                                                                                 Disclosure; Col 125-126; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU04289 standard; peptide; 100 AA.
              BAYU ) BAYLOR COLLEGE MEDICINE
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akakakakakakaka 78
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58.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                            Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   absent"
                                                                        WPI; 2001-049093/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 100 AA;
                                          Sottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Gaps

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Length 100; Indels 28 61

Zyskind JW; Xu HH;

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the invention fractions of a folder in the factor comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid confidence operably linked to the nucleic acid confidence operably linked to the nucleic acid confidence operably linked to the nucleic acid concentration is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated continued by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular continued for the polypeptide; (6) inhibiting cellular continued for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway continued for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a compound that inhibits in which the extent confount is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of proliferation of an organism. The antisense nucleic acids are quired for cellular proliferation of an organism. The antisense nucleic acids required for cellular proliferation or the isolate candidate molecules for rational decorations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYA--KKEKAYAKKAEKAA----KKAEAKAYK--AAEAKKKAKAEAKKYAKAAKAEKK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 144; DB 6; Length 428;
; Pred. No. 1.7e-05;
11; Mismatches 11; Indels 12;
                                                                                                            relates to an isolated nucleic acid comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant copolymer 1-77, myelin basic protein analogue.
                                                               Claim 25; SEQ ID NO 55748; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 --AAAEAAKKAAAAEKAAAEKAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 EYAAAEAKYKAEAA-KAAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR06445 standard; protein; 154 AA
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59.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 428 AA;
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for improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRRL B-L5910), a plasmid used to express Protein A.

The resulting plasmids encode fusion proteins consisting of beta-clucuronidase, Protein A, and rCOP-1 sequences. A methionine residue cocurs between the Protein A and rCOP-1 sequences, originating from the S. linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-77 contains oligonacleotide duplexes incoding the following segments: YKK, EAE, KAK, AAK, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the fusion protein. The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain amino acids. See also AAQ05665. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                       Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.9%; Score 142.5; DB 2
43.4%; Pred. No. 8.1e-06;
tive 10; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: December 14, 2004, 06:01:14 Job time : 86.1224 secs
                                                                                                                                                                                                                                                                                   Disclosure, Fig 11; 25pp; English.
                 89US-00312541.
90US-00473845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 43.4
                                                                            (REPK ) REPLIGEN CORP.
                                                                                                                                                           WPI; 1990-255848/34
                                                                                                                                                                                 N-PSDB; AAQ05664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 154 AA;
                   17-FEB-1989;
07-FEB-1990;
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Matches
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us-10-792-311-5.rapb

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December 14, 2004, 05:52:22 ; Search time 191.038 Seconds (without alignments) 143.965 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEKAYAKKAEKAAK......EAKYKAEAAKAAAKEAAYEA 77
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| Cgn2_6/ptodata1/1/pubpaa/US07_PUBCCMB.ppp:*
| Cgn2_6/ptodata1/1/pubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/1/pubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/1/pubpaa/US07_NEW_PUB.ppp:*
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| Cgn2_6/ptodata1/1/pubpaa/US08_PUBCCMB.ppp:*
| Cgn2_6/ptodata1/1/pubpaa/US08_PUBCCMB.ppp:*
| Cgn2_6/ptodata1/1/pubpaa/US08_PUBCCMB.ppp:*
| Cgn2_6/ptodata1/1/pubpaa/US08_PUBCCMB.ppp:*
| Cgn2_6/ptodata1/1/pubpaa/US09_PUBCCMB.ppp:*
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| Cgn2_6/ptodata1/1/pubpaa/US09_PUBCCMB.ppp:*
| Cgn2_6/ptodata1/1/pubpaa/US09_PUBCCMB.ppp:*
| Cgn2_6/ptodata1/1/pubpaa/US10B_PUBCCMB.ppp:*
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     version 5.1.6
- 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
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Maximum DB seq length: 200000000
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366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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Result No.	Score	* Query Match	% Query e Match Length DB I	08	a	Description
1	366	100.0	77	6	US-09-816-989A-5	Sequence 5, Appli
7	351.5			σ	US-09-816-989A-6	Sequence 6, Appli
٣	289		109	σ	US-09-816-989A-7	7
4	282.5			6	US-09-816-989A-4	Sequence 4, Appli
Ŋ	245.5	67.1	26	6	US-09-816-989A-3	m
9	150.5	41.1		15	US-10-282-122A-56483	Sequence 56483, A
7	148	40.4		15	US-10-282-122A-75047	Sequence 75047, A
80	146.5	40.0	387	15	US-10-282-122A-72645	Sequence 72645, A
6	146	39.9		15	US-10-282-122A-75772	Sequence 75772, A
10	144	39.3		15	US-10-282-122A-55748	Sequence 55748, A
11	142.5	38.9		15	US-10-282-122A-68109	Sequence 68109, A
12	141.5	38.7		15	US-10-282-122A-59321	Sequence 59321, A
13	141.5	38.7		14	US-10-127-032-120	Sequence 120, App

66237, A 8, Appli 16, Appl 67145, A 50, Appl 36, Appl 69962, A 78190, A	27, Appl 62547, A 64817, A 64817, A 61735, A 2, Appli 45264, A 67699, A	52, Appl 9889, Appl 9889, Appl 10710, Ap 197136, A 19716, A 10221, A 7, Appl 152005, 152005, 152015, 152015, Appl 1023, Appl
Sequence 66237, Sequence 8, Appl Sequence 16, App Sequence 67145, Sequence 50, App Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 78190,	Sequence 27, Appl Sequence 6247, P Sequence 64817, P Sequence 5, Appli Sequence 6173, P Sequence 45264, P Sequence 67699, P Sequence 67699, P	
US-10-282-122A-66237 US-09-820-843A-8 US-10-467-421-16 US-10-282-12A-67145 US-10-726-692-36 US-10-726-692-36 US-10-282-12ZA-6962 US-10-282-12ZA-6962 US-10-282-12ZA-6962	US-10-229-567-27 US-10-282-122A-64817 US-10-282-122A-64817 US-10-184-832-5 US-10-184-832-5 US-10-382-122A-61735 US-10-282-122A-45264 US-10-282-122A-6593 US-10-282-122A-6593 US-10-281-122A-6593 US-10-651-643-201	US-10-205-979-52 US-10-156-761-9889 US-10-156-761-9889 US-10-739-930-19712 US-10-739-930-19710 US-10-425-115-197135 US-10-437-963-193381 US-10-156-761-10221 US-10-181-071-7 US-10-437-963-152005 US-10-437-963-152005 US-10-425-115-198446 US-10-296-115-1023
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114 116 117 118 118 118 118	23 24 20 31 31 31	1

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doria
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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                   Sequence 5, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
US-09-816-989A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-816-989A-5
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APPLICANT: Lis, Dorison Title OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE TITLE OF INVENTION: AND FOR THERAPEUTIC USE TILL REPRENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT PILING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR PILING DATE: 1998-09-25 PRIOR PILING DATE: 1999-09-24 NUMBER OF SEQ ID NOS: 7 SOFTWARE: PACENTION NUMBER: POT/US99/22402 PRIOR FILING DATE: 1999-09-24 SEQ ID NOS: 7 SOFTWARE: PACENTIN VERSION 3.1 SEQ ID NO 4 LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 97/10599/22402
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-3
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                                                                                                                                                   61 YKAEAKKYAKAAKAEKKEYAAABAKKAEAAKAYKAEAAKAAAKEAAYEA 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.2%; Score 282.5; DB 9; Best Local Similarity 84.4%; Pred. No. 1.3e-17; Matches 65; Conservative 0; Mismatches 1;
                                                                                              37 -KAEAKKYAKAAKAEKKEYAAAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09816989A, Patent No. US20020115103A1, GENERAL INFORMATION: APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             US-09-816-989A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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US-09-816-989A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-6
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6
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Pred. No. 1.8e-23;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 109;
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Pred. No. 5.8e-18;
1; Mismatches 3;
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                                                                                                                                                Sequence 6, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
      61 YKAEAAKAAAKEAAYEA 77
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89.5%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 89.5'
Matches 77; Conservative
                                                                                              RESULT 2
US-09-816-989A-6
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US-09-816-989A-7
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US-10-282-122A-72645

Sequence 72645, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:
APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos
                                                                                                             US-10-282-122A-75047
; Sequence 75047, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
        190 AAALKKKAEAAEAAAEARKKA 211
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SEQ ID NO 75047
LENGTH: 407
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Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Ohlsen, Kari
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APPLICANT:
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-11-27
PRIOR PILING DATE: 2001-11-27
PRIOR PILING DATE: 2001-11-27
PRIOR PILING DATE: 2001-10-29
PRIOR PILING DATE: 2001-10-20
PRIOR PILING DATE: 2001-10-20
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR PILING PATE: 2001-02-16
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                                                                                                                                                                  ----AEAK 39
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Query Match 67.1%; Score 245.5; DB 9; Length 56; Best Local Similarity 72.7%; Pred. No. 1.7e-14; Matches 56; Conservative 0; Mismatches 0; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                               US-10-282-122A-56483
; Sequence 56483, Application US/10282122A
; Publication No. US20040029129A1
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity
Matches 44; Conserv
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LENGTH: 421
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                                                                                                 CURRENT APPLICATION NUMBER: 05/10/282,122A

CURRENT FILING DATE: 2003-02-20

FRICA PAPLICATION NUMBER: 60/191,078

FRICA PAPLICATION NUMBER: 60/191,078

FRICA PAPLICATION NUMBER: 60/206,848

FRICA PAPLICATION NUMBER: 60/207,727

FRICA PAPLICATION NUMBER: 60/207,727

FRICA PAPLICATION NUMBER: 60/230,335

FRICA PAPLICATION NUMBER: 60/230,335

FRICA PAPLICATION NUMBER: 60/230,335

FRICA PAPLICATION NUMBER: 60/230,347

FRICA PAPLICATION NUMBER: 60/230,347

FRICA PAPLICATION NUMBER: 60/242,578

FRICA PAPLICATION NUMBER: 60/242,578

FRICA PAPLICATION NUMBER: 60/253,625

FRICA PAPLICATION NUMBER: 60/253,625

FRICA PAPLICATION NUMBER: 60/257,931

FRICA PAPLICATION NUMBER: 60/257,931

FRICA PAPLICATION NUMBER: 60/257,931

FRICA PAPLICATION NUMBER: 60/257,931

FRICA PAPLICATION NUMBER: 60/267,636

FRICA REPLICATION NUMBER: 60/267,636

FRICA REPLICATION NUMBER: 60/267,636

FRICA REPLICATION NUMBER: 60/267,636

FRICA REPLICATION NUMBER: 60/267,636

FRICA PAPLICATION NUMBER: 60/26
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
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40.4%; Score 148; DB 15; Length 407;
Best Local Similarity 54.4%; Pred. No. 3.5e-05;
Matches 49; Conservative 8; Mismatches 13; Indels 20
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APPLICANT: Xu, H.,

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
FRIOR PILING DATE: 2000-03-21
FRIOR PILING DATE: 2000-05-23
FRIOR PILING DATE: 2000-05-23
FRIOR PILING DATE: 2000-05-26
FRIOR PILING DATE: 2000-05-26
FRIOR PILING DATE: 2000-09-06
FRIOR PILING DATE: 2000-09-06
FRIOR PILING DATE: 2000-09-06
FRIOR PILING DATE: 2000-09-06
FRIOR PILING DATE: 2000-10-23
FRIOR PILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2001-02-09
FRIOR FILING FILING DATE: 2001-02-09
FRIOR FILING FILI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 AAAEAKKKADAAAAKAAADAKKKAAAEKAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 AAAEAKYKAEAA------KAAAKEAA 74
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Sequence 55748, Application US/10282122A
CENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Andle, Carlos
APPLICANT: Andle, Chien, Kari
APPLICANT: Cyskind, Undith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamannco, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
SEQ ID NO 75772
LENGTH: 376
                                                                                                                             Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                        Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Salmonella typhi
US-10-282-122A-75772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-10-282-122A-55748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-05-23

PRIOR PELICATION NUMBER: 60/206,848

PRIOR PILING DATE: 2000-05-23

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/230,335

PRIOR PILING DATE: 2000-09-09

PRIOR PELING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PELING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PELING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-06

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PELING DATE: 2001-02-06

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PELING DATE: 2001-02-06

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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 AAEAKKKAEAEAAKAAADAKKKADAEA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 AAEAKYK--AEAAKAAA---KEAAYEA 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: MISC_FEATURE
; LOCATION: (303) .. (303)
; OTHER INFORMATION: X=any amino acid
US-10-282-122A-72645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (78)...(78)
OTHER INFORMATION: X=any amino acid
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Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                  Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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US-10-282-122A-75772
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LENGTH: 387
    APPLICANT
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20; Gaps

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1 AKKYAKKEKA-----YAKKAEKAAKKA---EAKAYKAAEAKKKAKAEAKKYA--- 44
                                          PRIOR FILING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-110-27
PRIOR PLICATION NUMBER: 60/253,625
PRIOR PLICATION NUMBER: 60/257,931
PRIOR PELICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2000-12-29
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR PILING DATE: 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.9%; Score 142.5; DB 15; Length 46.9%; Pred. No. 9.7e-05; tive 10; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 AKKKAAAEDAKKKAAEEAKKKAAADAQKKKAQEAARKA 245
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CURRENT APPLICATION NUMBER: 06/19/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-22

PRIOR PILING DATE: 2000-11-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PILING DATE: 2000-11-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PILING DATE: 2000-11-22
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                APPLICATION NUMBER: 60/230,347
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Ohlsen, Kari
Oylsend, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Pseudomonas putida
US-10-282-122A-68109
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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nes 46; Conserv
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Best Local S
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                                 CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-66

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2001-12-22

PRIOR PLING DATE: 2001-12-22

PRIOR PLING DATE: 2001-12-22

PRIOR PLING DATE: 2001-10-20

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-32
PRIOR FILING DATE: 2000-05-32
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 --AAAEAAKKAAAAEKAAAEKAA 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT:
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ORGANISM:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 120, Application US/10127032
| Sequence 120, Application US/10127032
| Publication No. US20030113742A1
| GENERAL INFORMATION:
| APPLICANT: Whiteley, Marvin
| APPLICANT: Dangera, M. Gita
| APPLICANT: Creahers, M. Gita
| APPLICANT: Creahers, Everett Peter
| TITLE OF INVENTION: BIOFILM FORMATION
| FILE REFERENCE: UIZ-070CP
| CURRENT APPLICATION NUMBER: US/10/127,032
| CURRENT APPLICATION NUMBER: US 60/285,190
| PRIOR PELING DATE: 2001-04-20
| PRIOR PELING DATE: 2001-04-20
| PRIOR PELING DATE: 2001-10-24
| NUMBER OF SEQ ID NOS: 170
| SEQ ID NO 120
| SEQ ID NO 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 59321
LENGTH: 323
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                                                                                                                                                                                                                          Length 323;
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Pred. No. 0.0001;
9; Mismatches 19; Indels
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
                                                                                                                                          ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-282-122A-59321
                                                                                                                                                                                                                        38.7%;
56.3%;
                                                                                                                                                                                                                        Query Match
Best Local Similarity 56.3
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45; Conservative
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113 KKAQQEAAKQA 123
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US-10-282-122A-66237
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US-10-127-032-120
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Sequence 8, Application US/09820843A

Publication No. US20030039963A1

GENERAL INFORMATION:
GENERAL INFORMATION:
ACCOMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REPRESENCE: 065915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 8
SEQ ID NO 8
SEQ ID NO 9
SEQ ID NO 9
SEQ ID NO 9
                                                                                                                                                  APPLICANT: Yanamouco, Koberc
APPLICANT: Yanamouco, Koberc
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERBNCE: ELITEA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-05-09
PRIOR PLING DATE: 2000-10-23
PRIOR PAPLICATION NUMBER: 60/230,347
PRIOR PAPLICATION NUMBER: 60/230,347
PRIOR PLING DATE: 2000-11-23
PRIOR PLING DATE: 2000-11-23
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,636
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PELING DATE: 2001-02-09
PRIOR PILING DATE: 2001-03-01
PRIOR DATE: 2001-03-01
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38.7%; Score 141.5; DB 15; Length 347;
Best Local Similarity 44.1%; Pred. No. 0.00011;
Matches 45; Conservative 9; Mismatches 19; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: H. influenzae
PEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: outer membrane integrity protein (tolA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 КККАКАБАККҮАКААКАБККЕУАААБАКҮКАБААКАААКБАА 74
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                                                                                  Carr, Grant
Yamamoto, Robert
Forsyth, R.
Wall, Daniel
Trawick, Joh
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; NAME/KEY: misc feature
; OTHER INFORMATION: gi|1573353
US-09-820-843A-8
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Query Match 38.5%; Score 141; DB 10; Length 372; Best Local Similarity 54.7%; Pred. No. 0.00013; Matches 47; Conservative 7; Mismatches 20; Indels 12; Gaps 4;

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52 KEYAAAEAKYKAEAAKAAAKEAAYEA 77 | | | | | | | | | | | | | | | | | 1 215 KAKAAAEAKAKADAEAKAATEAKRKA 240

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Search completed: December 14, 2004, 06:59:41 Job time: 191.038 secs

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Sequence 5, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 64, Appli
Sequence 64, Appli
Sequence 64, Appl
Sequence 64, Appl
Sequence 1355, Appli
Sequence 1355, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 21, Appli
Sequence 5169, Appli
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-405-743A-6
US-09-405-743A-7
US-09-405-743A-7
US-09-405-743A-3
US-09-405-743A-3
US-08-460-890A-64
US-08-460-890A-64
US-08-460-890A-64
US-08-460-91A-64
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US-09-115-746-2
US-09-115-746-2
US-09-543-681A-2
US-08-328-328-6321
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US-08-393-284A-2
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                                                                                                                                                                                                                                                                        478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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366
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                                                            OM protein
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Maximum DB
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No.
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Sequence 201, App Sequence 6, Appli Sequence 5, Appli Sequence 5, Appli Sequence 3, Appli Sequence 3, Appli Sequence 13743, A Sequence 13743, A Sequence 13743, A Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 132, Appl Sequence 141, Appl Sequence 18922, A Sequence 18922, A Sequence 18922, A Sequence 11, Appli Sequence 11, Appli		SHT MARKERS	Length 77; Indels 0; Gaps 0;	9	SHT MARKERS
US-09-205-426-201 US-08-993-008A-6 US-09-248-796A-26122 US-08-929-329-5 US-09-248-796A-26989 US-09-417-889-3 US-09-417-264-3 US-09-417-264-3 US-09-417-264-40 US-09-041-889-40 US-09-041-889-40 US-09-041-889-40 US-09-041-889-40 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-041-89-32 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-041-889-32 US-09-248-796A-18922 US-08-929-414-1	ALIGNMENTS	nn US/09405743A arch and Development Co., Ltd. GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS 77-A 1999-09-24 7 7 fer. 2.1 Sequence escription of Artificial Sequence: SYNTHE	Score 366; DB 4; L Pred. No. 7.2e-28; D; Mismatches 0;	arakaykaabakkkakabak 	on US/09405743A earch and Development Co., Ltd. GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS TUBS9-09-24 Tolumber 2.1 Sequence
22 1 2 56 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		43A-5 5, Application US/09405743A 5, 651493B INFORMATION: TT. Yeda Research and Devel TT. YEDA RESEARCH ON GLATIRAMER ACE TENENCE: 60807-A APPLICATION UNMER: US/09/4 FILING DATE: 1999-09-24 FILING DATE: 1999-09-24 FILING DATE: 1999-09-24 S: Patentin Ver. 2.1 5) S: Ratentin Ver. 2.1 NH. ARTHIFICIAL SEQUENCE NH: ARTHIFICIAL SEQUENCE SE SERVING NOSE TO SERVING NOSE T	100.0%; larity 100.0%; Conservative (AKKYAKKEKAYAKAEKA 	a
1. 2. 4. 6. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2.		i-743A-5 ie 5, Application US, No. 6514938 in Thrormation: ANT: Yeda Research OF INVENTION: GENTING ANTION: TRAPLICATION WUMBER TR FILING DATE: 1993; TOF SEQ ID NOS: 77 IRE: Patentin Ver.; NO 5 PRT HI: 77 PRT IISM: Artificial Seq RE: I TIPORMATION: DESCIT: I INFORMATION: DESCIT: I INFORMATION: DESCIT: I INFORMATION: DESCIT: I INFORMATION: DESCIT:	5 imi '	1 AKKYAKKE 	-743A-6 -e 6, Application US/(No. 6114938 No. 6114938 OF INFORMATION: OF INVENTION: GLATII REFERRACE: 60807-A RT APPLICATION NUMBER RY FILING DATE: 1999- ROF SEQ ID NOS: 7 RE: Patentin Ver. 2 NO 6 H: 86 H: 86 PRT ISM: Artificial Sequents
28 119.5 30 119.5 31 119.5 31 1113 31 1112 31 1112 31 1112 31 110.5 31 110.5 40 110.5 44 110.5 45 110.5 45 110.5 46 110.5 47 110.5 48 110.5		1 405-7 405-7 ence III NG ILICAN ILE OB E RENT RENT RENT TWAR ID NG ID N	S-09-405-743A-5 Query Match Best Local Sim Matches 77;	1 1 61 61	2 405-7 ence nt Nc RAL I LICAN LICAN LICAN LE OF RENT RENT RENT RENT ID NC NGTH: NGTH:
		RESULT US-09-01-09		\$ 40 A0	RESULT US-09-09-09-09-09-09-09-09-09-09-09-09-09-

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US-09-405-743A-3
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   SYNTHETIC
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Patent No. 6514938
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REPRENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TILLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS FILE REFERENCE: 60807-4
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO.7
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Pred. No. 1.7e-20;
1; Mismatches 3; Indels :
                                                                          Query Match

96.0%; Score 351.5; DB 4; Length
Best Local Similarity 89.5%; Pred. No. 1.9e-26;
Matches 77; Conservative 0; Mismatches 0; Indels
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US-09-405-743A-6
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OTHER INFORMATION: Description of Artificial Sequence:

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US-09-405-743A-7
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// OTHER INFORMATION: PEPTIDE
US-09-405-743A-4
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                                                                                                                                                                                                                             61 -----YKAEAAKAAKEAAYEA 77
                                                                                                                                                                                                                                                                61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                        . Sequence 7, Application US/09405743A ; Patent No. 6514938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 67.0
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                       RESULT 3
US-09-405-743A-7
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US-09-405-743A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 109
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                                                                                                                                  1 AKKYAKKEKAYAK-----AKKAEAK------AAKKAKAEAKKYAKAAKAEKKEYAAABAK 49
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                                                                                                     1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAABAKKKAKAEAKKYAKAAKAEKKEYAAAEAK
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                                                  11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS FILE REFERENCE: 60807-A
CURRENT APPLICATION WINBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 67.1%; Score 245.5; DB 4; Length 56; Best Local Similarity 72.7%; Pred. No. 1e-16; Matches 56; Conservative 0; Mismatches 0; Indels 2.
  Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WOO, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gritchalk, Stephen
TITLE OF INVENTION: NUTLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK------
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Score 282.5; DB 4;
Pred. No. 4.1e-20;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 64, Application US/08460890A Patent No. 5994109 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-405-743A-3
; Sequence 3, Application US/09405743A
; Patent No. 6514938
                                                                                                                                                                                                       77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
Query Match
77.2%;
Best Local Similarity 84.4%;
Matches 65; Conservative
                                                                                                                                                                                                       61 YKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YKAEAAKAAAKEAAYEA
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90071-2066
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1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
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APPLICANT: Woo, Savio L.C.
APPLICANT: Woo, Savio L.C.
APPLICANT: Gristiano, Richard J.
APPLICANT: Los ADRESS:
CORRESSES: Lyon & Lyon
STREET: Gristiano
CTTY: Los Angeles
CTTY: Los Angeles
COUNTRY: US A.A.ia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 39.5%; Score 144.5; DB 3; Length 100; Best Local Similarity 58.4%; Pred. No. 5.4e-07; Matches 45; Conservative 6; Mismatches 23; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be CTHER INFORMATION: present or absent.

US-08-167-641C-64
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/655,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WARDLEY, RICHART J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 64, Application US/08460971A
Patent No. 6150168
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APPLICATION NUMBER: 07/855,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08/167,641
                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || ||:| ||| || || 62 AKAKAKAKAKAKA 78
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                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
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Patent No. 6033884

GENERAL INPORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Stephen
TITLE OF INVENTION: WETHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Pifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 39.5%; Score 144.5; DB 2; Length 100; Best Local Similarity 58.4%; Pred. No. 5.4e-07; Matches 45; Conservative 6; Mismatches 23; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be CTHER INFORMATION: present or absent.

US-08-460-890A-64
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,890A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 20, 1992
APPLICATION NUMBER: PCT/0893/02725
FILING DATE: MARCH 19, 1993
ATTORNEY/AGENT INPORMATION:
NAME: WARDLEY, RICHARD J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: SIS" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
                                                                                                                                                                                                                                                                                                                            REFERENCE DOCKET NUMBER: 212/066
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 anino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE:
STRANDEDNESS: SIT
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US-08-167-641C-64
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3; Gaps

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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 64, Application US/08462040

Patent No. 6177554

GENERAL INFORMATION:

APPLICANT: Woo, Savio L.C.

APPLICANT: Gattiano, Richard J.

APPLICANT: Gottchalk, Stephen

ITILE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND

TITLE OF INVENTION: METHODS OF USE

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 39.5%; Score 144.5; DB 3; Length 100; Best Local Similarity 58.4%; Pred. No. 5.4e-07; Matches 45; Conservative 6; Mismatches 23; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-460-971A-64
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US33/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 212/063
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 anino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM COMDALIBLE
COMPUTER: IBM COMDALIBLE
SOFTWARE: FASTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTENG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: Unne 5, 1995
CLASSIFICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 акакакакакака 78
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MOLECULE TYPE: peptide
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US-08-462-040-64
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.5%; Score 144.5; DB 3; Length 100; Best Local Similarity 58.4%; Pred. No. 5.4e-07; Matches 45; Conservative 6; Mismatches 23; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be ; OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-252-991A-29581

Sequence 29581, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-489-039A-13565
; Sequence 13565, Application US/09489039A
Parent No. 6610836
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEKAYAKKAEKAAKKAEAKA
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29581
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                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
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Sequence 8, Application US/09115746

Patent No. 6228601

GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Can's Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 36.6%; Score 134; DB 3; Best Local Similarity 52.0%; Pred. No. 3.6e-05; Matches 39; Conservative 9; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85326/102/DRLO
                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547 TKVAEAEKQKAAEAA 561
                                                                                                          547 TKVAÉAEKQKAAEAA 561
                                                                  60 KYKAEAAKAAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 KYKAEAAKAAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORWATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-405-743A-2
                                                                                                                                                                               RESULT 13
US-09-115-746-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-115-746-8
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PLING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13565
                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 EQAAAKAAADAKKQAEAAAAKAAAEAKKQAEAEAAK--AAAEAQKKAEAAAKKAQQEAE 262
                                                                                                                                                                                                                                                                                                                                                                                                                             8 EKAYAKKAEKAAKKAEAKAYK-AAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAA 66
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Patent No. 5876734

GENERAL INFORMATION:

GENERAL INFORMATION:

TAPLICANT: Kirchhoff, Louis V.

APPLICANT: Otsu, Keiko

TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION

TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                        DB 4; Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 134; DB 2; Length 643;
Pred. No. 3.6e-05;
9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: 0.2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/POCKET NUMBER: 29,768
REFERENCE/POCKET NUMBER: 29,768
TELEPRAK: (2021672-5300
TELEPRAK: (2021672-5300
TELEPRAK: (2021672-5399
                                                                                                                                                                                                                                                                                                                                     Score 141.5; DB 4
Pred. No. 5.1e~06;
9; Mismatches 19
                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                     38.7%;
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INFORMATION FOR SEQ ID NO: 8:
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Best Local Similarity 52.0%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 643 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 56.3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 KKAQQEAAKQA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-216-894-8
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US-08-216-894-8
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA
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Parent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GATTIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
23; Indels
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us-10-792-311-5.rai

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318 ATKVABABK---QKAABATKVABABKQKAABATKVABABKQKAABETKOKAABETKVABABKA 374
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                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHEFIC
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-2
                                                                                                                                                                                                                                                                                                                                                                 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08216894
| Patent No. 5876734
| GENERAL INFORMATION:
| APPLICANT: Kirchhoff, Louis V. APPLICANT: Kirchhoff, Louis V. TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
| TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
| NUMBER OF SEQUENCES: 10
| CORRESPONDENCE ADDRESS: ADDRESSE: Foley & Lardner
                                                                                                                                                                                                                                                                                                            Query Match 35.8%; Score 131; DB 4; Length 45; Best Local Similarity 50.6%; Pred. No. 4.4e-06; Matches 39; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR.1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKK-----AKAEKA-----KKAYKAAEAKKAAKYE
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELDERAX: (202/)
TELBERAX: 904136
INFORMATION FOR SEQ.
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acids
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 -KAAAEKAAAKEAAYEA 45
                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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US-08-216-894-10
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                   Copyright
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- protein search, using sw model OM protein

Run on:

December 14, 2004, 05:47:53 ; Search time 19.7764 Seconds (without alignments) 418.411 Million cell updates/sec

US-10-792-311-6

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
-	164	40.1	421	2	JV0057	tolA protein - Esc
8	157.5	38.5	376	~	AG0592	tolA protein (impo
٣	156.5	38.3	1701	~	T09127	probable erythrocy
4	155	37.9		~	F90725	membrane spanning
S	155	37.9	394	~	G85576	membrane spanning
9	154	37.7	347	~	E83525	Tola protein PA097
7	151	36.9	210	~	A25550	histone H1 - sea u
80	149	36.4	231	~	859589	histone H1 - Chlam
σ	147.5	36.1	388	7	AC0138	TolA colicin impor
10	147	35.9	214	0	G70673	ш
11	144	35.2	211	N	A28100	histone H1-beta, e
12	142.5	34.8	344	N	834153	mst101-1 protein -
13	142	34.7	372	~	G64064	outer membrane int
14	140.5	34.4	328	7	A44993	cytosolic repetiti
15	140.5	34.4	1390	7	S51364	sperm tail-specifi
16	138	٠	217	~	A26721	histone H1-gamma,
17	137.5	33.6		7	T30296	R27-2 protein - Tr
18	135	33.0		7	E60110	repetitive protein
19	134	32.8		7	809388	histone H1 - sea u
20	133.5	32.6		~	B43592	outer membrane pro
21	133.5	32.6		~	S25194	, ye
22	132.5	32.4		Н	HSTRIR	histone H1 - rainb
23	132	32.3	248	Н	HSUR1P	H,
24	131	32.0		~	T23778	H1.1
25	130.5	•		~	A28456	histone H1.10 - ch
26	130.5	31.9		7	AE1689	hypothetical prote
27	129.5	31.7	924	~	T06636	hypothetical prote
28	129.5	31.7	1403	7	T11583	s transla
29	129	31.5	218	~	A23055	histone H1.01 - ch

N RESULT AG0592

hypothetical prote	nistone Hi - musco	histone H1-II - Vo	histone H1 (clone	cgcr-4 protein - C	histone H1 (clone	histone H1.02 - ch	histone H1.03 - ch	conserved hypothet	hypothetical prote	histone H1 homolog	histone H1.11L - c	tolA protein VC183	histone H1B - Afri	histone H1B - Afri	hypothetical prote
T17698	201762	JN0748	T06241	S19113	T06257	HSCH1	D28456	E75383	T06635	S61926	B28456	A82152	HSXL1B	I51447	T22455
01 0	N (C)	~	0	~	-	7	~	N	7	~	~	Н	~	7
311	218	241	284	265	288	218	224	581	606	182	225	356	219	220	581
31.2	30.9	30.9	30.9	30.8	30.8	30.7	30.7	30.6	30.4	30.3	30.2	30.1	30.0	30.0	30.0
127.5	126.5	126.5	126.5	126	126	125.5	125.5	125	124.5	124	123.5	123	122.5	122.5	122.5

ALIGNMENTS

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CyGocies: Escherichia coli (strain K-12)

CySpecies: Escherichia coli

CyCoste: 07.58p-1990 #sequence

CyAccession: 470057; B64810

N; Reference number: Nuo1657; MUID: 90078104; PMID: 2687247

A; Reference number: JV0057; MUID: 90078104; PMID: 2687247

A; Reference number: JV0057; MUID: 90078104; PMID: 2687247

A; Reference number: JV0057; MUID: 90078104; PMID: 2687247

A; Residues: 1-421 cLEV>

A; Residues: 1-421 cLEV>

A; Rose, D.J.; Mau, B.; Shao, Y.

A; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Reference number: A64720; MUID: 97426617; PMID: 9278503

A; Recension: B64810

A; Recidues: 1-421 cleub;
A; Residues: 1-421 cle
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A;Gene: tolA
A;Map position: 17 min
A;Start codon: GTG
C;Keywords: nucleotide binding; P-loop; transmembrane protein
E;14-34/Domain: transmembrane #status predicted <MSS>
F;78-301/Domain: helical #status predicted <HSR>
F;355-362/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Indels
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Best Local Si
Matches 51
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ch 37.9%;
l Similarity 53.1%;
51; Conservative (
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Best Local Similarity
Matches 51; Conserv
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A, Status: preliminary
A, Molecule type: DNA
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tolA protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT16 C;Species: Salmonella enterica subsp. enterica serovar Typhi (strain CT16 A;Note: this species has also been called Salmonella typhi (species has also been called Salmonella typei (species has also been called Salmonel) and text. Cannerton, P.; Cronin, A.; Davis, N.; Pickard, D.; Wain, J.; Churcher, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
N;Ruthers: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: AB0502; MUD:21534947; PMID:11677608
A;Reference number: AB0502; MUD:21534947; PMID:11677608
A;Reference by A;Refere
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membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-U1-2001 #sequence_revision 18-Ju1-2001 #text_change 09-Ju1-2004
C;Accession: F90725
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R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
A;Accession: T09127
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A,Cross-references: GB:AL513382; PIDN:CAD05209.1; PID:g16501979; GSPDB:GN00176
C;Genetics: AYV0793
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A;Introns: 62/1; 1648/1; 1674/2; 1697/1
C;Keywords: alternative splicing; cell binding; erythrocyte invasion
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k; Pred. No. 0.00014;
10; Mismatches 17; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.3%; Score 156.5; DB 2; Length 1
53.5%; Pred. No. 0.00052;
iive 9; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 AAEAKKKAEAEAAKAAADAKKKADAEAAKAAE 217
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54.8%;
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Matches 53; Conservative
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Best Local Similarity
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R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G., gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: F90725
A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-394 <HAY>
A; Cross-references: UNIPROT:08X965; GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GP-A; Cross-references: etrain O157:H7, substrain RIMD 0509952
A; Genetics:
A; Genetics:
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C;Genetics:
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Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc A;Accession: E83225
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grobbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E83525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 155; DB 2;
Pred. No. 0.00022;
6; Mismatches 23;
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC013
R;Parkhil, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; Accession: AC013
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; A.B.; Parkhill, J; Wren, B.W.; Simmonds, M.; Skelton, J.; Stevens, R.M.; Davis, P.; Dougan, G.; Inl, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, R.; Whitehead, S.; Barrell, I. Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; WUID:21470413; PMID:11586360
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A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT: Q8ZGZ2; GB: ALS90842; PIDN: CAC89966.1; PID: g15979190; GSPDB: GR
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A;Authors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TolA colicin import membrane protein [imported] - Yersinia pestis (strain CO92)
                                                                                                                                                                                                                                                                                                                                                              214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C,Accession: G70673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 KEKAYAKKAEKAAKKAEAKAYK----AAEAKKKAKAEAKKYAKAAKAEKKE------
A;Residues: 1-173,'P',174-231 <FAW>
A;Cross-references: EMBL:U16726; NID:g571479; PIDN:AAA98452.1; PID:g571480 C;Genetics: A;Introns: 62/3; 101/3 A;Introns: 62/3; histone H1 C;Superfamily: histone H1 C;Keywords: chromosomal protein; DNA binding; nucleosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                      36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---AEAKYKAEAAKKAYKAEAAKAAAKEAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 EVAEKAAADAAEKKAAAADKKKAAAAKKYAAAAEAKKKAAAAEAA 258
                                                                                                                                                                                                                                                                   29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 ------YAAAEAKYKAEAAKK-AYKAEAAKAAAKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable hupB - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                        Match 36.4%; Score 149; DB 2; Local Similarity 39.5%; Pred. No. 0.00038; les 47; Conservative 7; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 KEYAA-----
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Best Local Similarity
Matches 47; Conserv
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A; Residues: 1-214 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <KUR>
                                                                                                                                                                                                              Query Match
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Matches
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histone H1 - sea urchin (Lytechinus pictus)
Cispecies: Lytechinus pictus (painted urchin)
Cispecies: Lytechinus pictus (painted urchin)
Cipacies: Jytechinus pictus (painted urchin)
Cipacession: A25550
R;Knowles, J.A.; Childs, G.J.
R;Knowles, J.A.; Childs, G.J.
A;Klowles, J.A.; Childs, G.J.
A;Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus an A;Reference number: A25550; MUID:87040778; PMID:3022245
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histone H1 - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S59589; S62122
C;Accession: S59589; S62122
Curr. Genet: 28, 333-345, 1995
A;Title: The organization structure and regulatory elements of Chlamydomonas histone gen
A;Reference number: S59581; MUID:96120862; PMID:8590479
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A; Cross-references: UNIPROT: Q39576; EMBL: U16726
A; Cross-references: UNIPROT: Q39576; EMBL: U16726
A; Note: the authors did not translate the codon for residue 1
R; Fabry, S.; Ford, C.; Lindauer, A.; Mueller, K.; Cornelius, T.; Schmitt, R.
submitted to the EMBL Data Library, October 1994
A; Description: The organization, structure and controlling elements of Chlamydomonas his
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Essidues: 1-347 <570>
A;Cross-references: UNIPROT:P50600; GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG0436
A;Experimental source: strain PAO1
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-210 <KNO>
A;Residues: 1-210 <KNO>
A;Cross-references: UNIPROT:P06144; GB:X04488; NID:g9616; PIDN:CAA28177.1; PID:g9617
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
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                                                                                                                                                                                                                                                                                                                                                                 44
                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKAYAKKAEKAKKAEAKAYKAA------EAKKKAKAKAEAKKYA---
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                                                                                                                                                                                                                                                                                                      21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 KKKAAEEAKKKAAAEAAKKKAAVEAAKK--KAAAAAAARKAA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 --KAAKAEKKEYAAAEAKYKA--EAAKKAYKAEAAKEAA 83
                                                                                                                                                                                                                                          Score 154; DB 2;
Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                      11; Mismatches
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A, Status: nucleic acid sequence not shown
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Matches 46; Conservative
                                                                                                                                                                                                                                                                                                         49; Conservative
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Best Local Similarity
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A,Accession: JC5212
A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: V',2-47,'A',49-141,'R',143-164,'P',166-189,'R',191-202,'A',204-226,'A',228-2
A,Cross-references: GB:U32470
A,Experimental source: strain 1479
A,Experimental source: strain 1479
A,Note: the authors translated the codon CGT for residue 190 as Ala
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Cybosolic repetitive antigen - Trypanosoma cruzi
Cybosolic repetitive antigen - Trypanosoma cruzi
Cybosolic - Trypanosoma cruzi
Cybosolic - Trypanosoma cruzi
Cybosolic - Trypanosoma cruzi
Cybosolic - Trypanosoma cruzi
Rybafalle, July; Linss, July - Krieger, M.A.; Souto-Padron, T.; de Souza, W.; Goldenberg, & Mol. Biochem. Parasitol. 35, 127-136, 1989
Mol. Biochem. Parasitol. 36, 1989
Mol. Biochem. Parasitol. 37, 1989
Mol.
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A;Mactus: mucleic acid sequence not shown; translation not shown
A;Mactus: mucleic acid sequence not
A;Mactus: 1-372 acIGR>
A;Cross-references: UNIPROT:P44678; GB:U32722; GB:L42023; NID:g1573348; PIDN:AAC22041.1;
R;Sen, K.; Sikkema, D.J.; Murphy, T.F.
A;Title: Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA ar
A;Reference number: JC5212; MUID:97080550; PMID:8921895
                                                                                                                                                                                                                                                          Outer membrane integrity protein tolA - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: G64064; JC5212
C;Accession: G64064; JC5212
M.D.; Multe, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Frandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Reference number: A64000; MUID:95350630; PMID:7542800
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Pred. No. 0.0017;
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Best Local Similarity
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A; Start codon: GTG
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C;bate: 28-Aug-1389 #sequence_revision 28-Aug-1389 #text_change 09-Jul-2004
C;Accession: A28100
A;Elai, Z.C.; Childs, G.
Mol. Cell. Biol. 8, 1842-1844, 1988
A;Title: Characterization of the structure and transcriptional patterns of the gene encols, A;Reference number: A28100, MUID:88246461; PMID:2837660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAAKAEKKEYAAAEAK 60
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C;Species: Drosophila hydei
C;Species: Drosophila hydei
C;Abate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34153
R;Neesen, J.; Heinlein, U.A.O.; Buenemann, H.
submitted to the EMBL Data Library, June 1993
A;Reference number: S34153
A;Reference number: S34153
A;Reteus: preliminary
                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKKAEKAAKKAEAK-----AYKAAEAKKKAKAEAKKYAKAAKKEY
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-211 <LAI>
A;Cross-references: UNIPROF:P15869; GB:M20314
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; embryo; nucleosome; nucleus
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A;Gene:PyBase:Dhyd/mst101
A;Cross-references: PlyBase:FBgn0011816
C;Superfamily: neurofilament triplet H protein
                                                                                                                                                                                                      10;
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                                                                                                                             Length 214;
                                                                                                                                                                                                 34; Indels
                                                                                                                 Score 147; DB 2;
Pred. No. 0.0005;
3; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 TKAVKKTAVKASVRKAATKAPAKKAAKRPATKA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                55 AAAEAK--YKAEAAKKAYKAEAAKAAAKEAAYEA 86
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                                                                                                                 Query Match 35.9%;
Best Local Similarity 50.0%;
Matches 47; Conservative
A;Gene: hupB
C;Superfamily: histone H1
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es 49; Conserv
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A; Residues: 1-344 <NEE>
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Species: Drosophila hydei
C;Species: Drosophila hydei
C;Accession: S51364; S14154
R;Neesen, J:; Padmanabhan, S.; Buenemann, H.
Eur. J. Biochem. 225, 1089-1055, 1994
A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represe lpha-helical rods within the extremely elongated spermatozoa of Drosophila hydei.
A;Reference number: S51364; MUID:95045538; PMID:7957199
A;Reference number: S51364; MUID:95045538; PMID:7957199
A;Reference number: S51364; MUID:95045538; PMID:7957199
A;Residues: 1-1390 «NEE>
A;Cross-references: UNIPROT:Q08696; EMBL:X73481
B;Neesen, J:; Heinlein, U.A.O.; Buenemann, H.
Submitted to the EMBL Data Library, June 1993
A;Reference number: S34153
A;Reference number: S34153
A;Reference number: S34154
A;Molecule type: DNA
A;Residues: 1-163, 'E',164-236,'Q',237-254,257-320,'E',321-1390 «NEW>
A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
C;Genetics: Genetics: FlyBase:FBgn0011816
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2 KKYAKKEK--AYAKKAEKAAKKAE--AKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAA 57
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34.4%; Score 140.5; DB 2; Length 1390;
Best Local Similarity 51.8%; Pred. No. 0.006;
Matches 44; Conservative 4; Mismatches 32; Indels 5;
                                                                                                                                             167 TKVAEAEKQKAAEATKVAEAEKQKAAEA 194
                                                                                                     60 KYKAEAAK-KAYKAEAAKAAAKEAAYEA 86
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Search completed: December 14, 2004, 05:52:15 Job time: 20.7764 secs

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Q9cm70 pasteurella
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Q88ni6
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P19934
version 5.1.6
- 2004 Compugen Ltd.
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                                                                                                                                                                           1825181 seqs, 575374646 residues
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007RC08
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TOLA ECOLI
098W16
0088N16
07C204
0813A1
06D7F3
06D7F3
06D7F3
06D7F3
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Maximum Match 100%
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CAE80819
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074W64
AAS61283
Q6CDX0
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098KG7
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Gapop 10.0 , Gapext 0.5
 GenCore (c) 1993
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Match Length DB
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Q8zgz2 yersinia pe
Q8zzz8 yersinia pe
Q9xbl8 mycobacteri
P95109 mycobacteri
Q7n6t7 photorhabdu
Q7558 plasmodium
Aaq7346 plasmodium
Aaq7346 plasmodium
Ag71466 plasmodium
Q8t5c8 plasmodium
Q6t986 acinetobact
Q6n8x8 rhodopseudo
Cae77215 rhodopseu
Q08695 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P., McClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P., McClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P., Lourney L., Porvollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney B., R. Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Matereton R., Wilson R.K.; Miller W., Stoneking T., Nhan M., L. L.Z., LTZ., Spieth Sequence of Salmonella enterica serovar Typhimurium C. LTZ., Nature 413:852-856(2001).

R EMBL, AROSPISTO, ALL9691.1; -. REMBL, AROSPISTO, IPRO10528; Tola.

R InterPro; IPR010528; Tola.

R Pani, PP06519; Tola.

R Complete proteome.

W Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Gaps
                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tol protein, membrane spanning protein.
Mame=cola, orderedLocusNames=STM0747;
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86
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01-MRR-2004 (TrEMBLrel. 26, Created)
01-MRR-2004 (TrEMBLrel. 26, Last sequence update)
10-MRR-2004 (TrEMBLrel. 26, Last annotation update)
Brythrocyte binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
40.5%; Score 165.5; DB 2;
Best Local Similarity 51.9%; Pred. No. 0.00018;
Matches 55; Conservative 14; Mismatches 16;
                                                                                                                                                                                                                                                        407 AA
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                      DBH MYCBO
DBH MYCTU
Q7N6T7
                                                                                                                                                           MST1 DROHY
                                                           Q7K5Q8
AAQ73467
Q7K5Q7
AAQ73466
Q8T5C8
                                                                                                                                QGNBX8
CAE27215
                                                                                                                                                                                                                                                                                Created)
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MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                (TrEMBLrel. 20,
                                                                                                                                                                                                                                                        PRELIMINARY;
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 388
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344
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 NCBI_TaxID=602;
                                                                                                                                                                                                                                                                               01-MAR-2002
 147.5
147.5
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Q7RC08
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  Q8ZQT6
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Lloubes R.;
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                                                                                                                                                                                                                                                                                                                      Carucci D.J.;
"Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelli yoelii.";
Nature 419:512-519(2002).
                                                                                                                                  Silva J.C., Ermolaeva M.D., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Koeack D.S., Shunway M.F., Blüwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAINSIZE / JMIGS,
STRAINSIZE / JMIGS,
STRAINSIZE / JMIGS,
LEVENDOOG S.K., Webster R.E.;
"Nuclectide sequences of the tola and tolb genes and localization of their products, components of a multistep translocation system in Escherichia coli.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                 CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=tolA; Synonyms=cim, excC, lky; OrderedLocusNames=b0739;
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1701;
                      Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                        52 KEYAAA----EAKYKAEAAKKA----YKAEAAKAAAKE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.3%; Score 165; DB 2; 56.1%; Pred. No. 0.00064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
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Plasmodium yoelii yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                         NCBI_TaxID=73239;
                                                                                                   STRAIN=17XNL;
PubMed=12368865;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tola protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.;
Filamentous Biage infection: crystal structure of g3p in complex with
its coreceptor, the C-terminal domain of TolA.";
Structure 7:711-722(1999)
-!- FUNCTION: Involved in the tonB-independent uptake of group A
colicins (colicins A, El, E2, E3, and K). Necessary for the
colicins to reach their respective targets after initial binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Periplasmic (Potential).
DOMAIN II (ALDHA-HELICAL).
DOMAIN III (FUNCTIONAL).
13 tandem repeats of [EDA]-K(1,2)-A(2,4).
2.
                                                                                                                                      STRAIN-K12;
MEDLINE=97061202; PubMed=8905232;
Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Oshima T., Alba H., Baba T., Kajihara M., Kanai K., Kashimoto K., Inada T., Itoh T., Kajihara M., Kani T., Mizobuchi K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacteriophage DNA. SUBUNIT: Interacts, via domain II, with porins ompC, phoE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Levengood S.K., Beyer W.F. Jr., Webster R.E.;
"TolAs membrane protein involved in colicin uptake contains an
extended helical region.";
Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                               "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Derouiche R., Gavioli M., Benedetti H., Prilipov A., Lazdunski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "TolA central domain interacts with Escherichia coli porins.";
EMBO J. 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the bacteria. Also involved in the translocation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inner membrane; Protein transport; Repeat; Transmembrane; DOWAIN 1 13 Cytoplasmic (Potential). TRANSMEM 14 34 Potential.
"The complete genome sequence of Bscherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF06519; TolA; 1.
3D-structure; Bacteriocin transport; Complete proteome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99332679; PubMed=10404600;
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MEDLINE=91296736; PubMed=2068069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH PORINS.
MEDLINE=97133271; PubMed=8978668;
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EMBL; D90713; BAA35405.1; -.
PIR; JV0057; JV0057.
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EchoBASE; EB1000; --.
EcoGene; EG11007; tolA.
InterPro; IPR010528; TolA.
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GO; GO: 0016020; C: membrane; IEA.
GO; GO: 0016020; C: mucleosome; IEA.
GO; GO: 0000786; C: nucleosome; IEA.
GO; GO: 0000534; C: nucleous; IEA.
GO; GO: 0000584; C: periplasmic space (sensu Gram-negative Bact. . .; IEA.
GO; GO: 0003677; F: DNA binding; IEA.
GO; GO: 0006334; P: protein transporter activity; IEA.
GO; GO: 0006334; P: nucleosome assembly; IEA.
GO; GO: 0015031; P: protein transport; IEA.
InterPro; IRR005819; Histone—H5.
InterPro; IRR005829; TolA.
InterPro; IRR005820; TolA.
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GO; GO:000786; C:nucleosome; IEA.
GO; GO:0005634; C:nucleosome; IEA.
GO; GO:0016289; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
GO; GO:0003677; P:DNA binding; IEA.
GO; GO:0008565; F:protein transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinke L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F., Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M., Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K., Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas putida (strain KT2440).

Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae; Pseudomonas.

MCBI_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 372;
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                                                                                                                                                                                                                                                                                                                                                                                                          39.9%; Score 163; DB 2; Length 37 53.1%; Pred. No. 0.00025; ive 12; Mismatches 22; Indels
                                                 Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; X74218; CABS0780.1; -.
HSSP; P50600, 1LR0.
                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0624; HISTONEH5.
TIGRFAMB; TIGR01352; tonB_Cterm; 1.
SEQUENCE 372 AA; 40133 MW; 87F49785ECC3COBC CRC64;
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Name=tolA; OrderedLocusNames=PP1221;
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MEDLINE=22423060; Pubmed=12534463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96422022; PubMed=8824639;
Rodriguez-Herva J.J., Ramos J.;
"Characterization of an OprL null mutant of Pseudomonas putida.";
J. Bacteriol. 178:5836-5840(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Indels 10;
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Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.1%; Score 164; DB 1; Length 421; 59.3%; Pred. No. 0.00024;
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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                              43156 MW; 8B2F52B4B97C655E CRC64;
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Last sequence update)
Last annotation update)
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RKKAATEAAEKA-KAEAEKKAAAEKA 232
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MEDLINE=96198174; PubMed=8626299;
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                                 NCBI_TaxID=303;
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DISULFID
HELIX
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134 AEVAAAKAAADAKAAEBAAKKAAADAKKKAEAEAAKAAAEAQKKAEVAAAALKKKAEAAE 193
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Bell K.S., Sebainia M., Pritchard L., Holden M., Hyman L.J.,
Bell K.S., Sebainia M.R., Bentley S.D., Churcher C., Mungall K.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Barrell B.G., Parkhill J., Toth I.K.;
Submitteed (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BX950851; CAG74282.1;
SEQUENCE 395 AA; 41698 MW; 2DBIDAA64E984199 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AKKEKAYAKKAEKAAKKAEAKAYK----AAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK
                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN=301 / Serotype 2a;

MEDLINE=22272406; PubMed=12384590;

Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,

Jin O., Yuan F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,

Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,

Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441 (2002).
EMBL; AE015086; AAN42202.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erwinia carotovora subsp. atroseptica SCRI1043.
Bacteria, Proteobacteria, Gammaproteobacteria; Enterobacteriales;
           Membrane spanning protein, required for outer membrane integrity.
Name=tolA; OrderedLocusNames=SF0558;
Shigella flexneri.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 39.6%; Score 162; DB 2; Best Local Similarity 56.5%; Pred. No. 0.00032; Matches 52; Conservative 7; Mismatches 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae, Pectobacterium
NCBI_TaxID=218491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2004 (TrEMBLrel. 28, 01-OCT-2004 (TrEMBLrel. 28, 01-OCT-2004 (TrEMBLrel. 28,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P19934; 1TOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                        NCBI_TaxID=623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tola protein.
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Q6D7F3
              요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKA--YAKKAE-KAAKKAEAKAYKAA--EAKKKAKAEAKKYA-----KAAKA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAA----KAEKKE
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-2457T;
MEDLINE-22590274; PubMed=12704152;
MEDLINE-22590274; PubMed=12704152;
Mei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Wei J., Goldberg M.B., Plunkett G. III, Rose D.J., Darling A.,
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative genomics of Shigella
fleaneri serotype 2a strain 2457T.";
Infect. Immun. 71:277-2786(2003).
EMBL; AE016979; AAP16075.1;
InterPro; IRR010228; TolA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
NCBI_TaxID=623;
                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                       39.9%; Score 163; DB 2; Length 372; 53.1%; Pred. No. 0.00025; ive 12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.6%; Score 162; DB 2; Length 413; 56.5%; Pred. No. 0.00032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Indels
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                                                                                                                                                                                                                                                                  372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 AKKKAAAEDAKKKAAEEAKKKAAADAQKKKAQEAARKA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 EKKEYAAAEAKYK-AEAAKKAYKAEAAKAAAKEAAYEA 86
GO; GO:0006334; P:nucleosome assembly; IEA.
GO; GO:0015031; P:protein transport; IEA.
InterPro; IPR005819; Histone_H5.
InterPro; IPR016528; TolA.
InterPro; IPR016528; TolA.
PRINTS; PR0654; HISTONEH5.
TIGRPAMS; TIGRAMS; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 AA
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Name=tolA; OrderedLocusNames=S0571;
Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                               52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52; Conservative
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                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 372 AA;
                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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01-JUN-2003
01-MAR-2004
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Q83SA1;
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07C204;
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Q7C2Q4
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Q83SA1
ID Q83S
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Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.; "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.",
                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-AAEAKKKAKAKAEAKKYA----KAAKAEKKEYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAYA----KKAEKAAKKAEAKAYKAAEAKKKAKA----EAKKYAKAAK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Indels 19; Gaps
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi (T18."; Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kappe S.H., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.; "A family of chimeric erythrocyte binding proteins of malaria parasites.";
                                                                                                                                                                                                                                                                                                                                     DB 2; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kappe S.H.I., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF031986; AAQ73456.1; -.
SEQUENCE 1652 AA; 193757 MW; 8567E6E558B3F75C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams J.H.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                     376 AA; 38804 MW; EC21F2C4767A8A42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                     38.5%; Score 157.5; DB 2;
54.8%; Pred. No. 0.00063;
cive 10; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           roc. Natl. Acad. Sci. U.S.A. 95:1230-1235(1998)
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53.5%; Pred. No. 0.0025;
live 9; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 ААБАКККАБАБААКАААРАКККАЛАБААКАААБ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 AAEAKYKAEA-----AKKAYKAEAAKAAAK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1652 AA.
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                                                               SEQUENCE FROM N.A.
STRAIN-TY2 / ATCC 700931;
MEDLINE-22531367; Pubmed=12644504;
                                                                                                                                                                                 J. Bacteriol. 185:2330-2337(2003).
EMBL; AL627268; CAD02209.1; -.
EMBL; AL641841; AAO69743.1; -.
HSSP; P19934; ITOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98115903; PubMed=9448314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Erythrocyte binding protein
                                                                                                                                                                                                                                                      TolA.
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nes 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium yoelii yoelii
                                                                                                                                                                                                                                                   InterPro; IPR010528;
Pfam; PF06519; TolA;
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                                                                                                                                                                                                                                                                                     Complete proteome SEQUENCE 376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=73239;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davis R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                               FIRAIN=06:HI / CFT073 / ATCC 700928;

MEDLINE=2238234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

EMBL; AE016757; AAN79291.1;

HSSP; P19934; ITOL.
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                                                                                                                                                                                                             Excherichia coli 06.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 160; DB 2; Length 421;
Pred. No. 0.00046;
7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 AA; 43184 MW; DB296626F056D385 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    028801; 0708P3;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
193 EKAAEAAKQKAAETAKAEAAKAAA-EAAKEA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=tolA; OrderedLocusNames=STY0793, t2129; Salmonella typhi.
                                                                                                    421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 KYKA--EAAKKAYKAEAAKAAAKEAA 83
                                                                                                                                                                                                 Name=tolA; OrderedLocusNames=c0818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.1%;
58.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR010528; TolA. Pfam; PF06519; TolA; 1. Complete proteome.
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nes 50; Conservative
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SEQUENCE FROM N.A.
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STRAIN=YM;
Kappe S.H.I., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                          (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium yoelii yoelii
                                                                                                                                                                  Best Local Similarity
[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                               02-MAR-2004
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02-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 38.3%; Score 156.5; DB 2; Length 1652; Local Similarity 53.5%; Pred. No. 0.0025; No Sai, Conservative 9; Mismatches 18; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98115903; PubMed=9448314;
Kappe S.H., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.;
"A family of chimeric erythrocyte binding proteins of malaria
parasites.";
                                                                                                                                                                                                                                                        Kappe S.H., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.; "A family of chimeric erythrocyte binding proteins of malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Erythrocyte binding protein 4 (Brythrocyte binding protein 2)
                                                                                                                                                    Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium;
Plasmodium yoelii.
NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                  Kappe S.H.I., Noe A.R., Fraser T.S., Blair P.L., Adams J.H., Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium yoelii yoelii.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBL_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                        Adams J.H.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF031886; AAQ73456.1; -.
SEQUENCE 1652 AA; 193757 WW; 8567E6E558B3F75C CRC64;
                         81
            49 AEKKEYAA--AEAKYKAEAAKKA----YKAEAAKAAKE 81
                                                                                         02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
Erythrocyte binding protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 AEKKEYAA--AEAKYKAEAAKKA---YKAEAAKAAAKE
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                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 95:1230-1235(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1680 AA.
                                                                                        1652 AA
                                                                                        PRT;
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                                                                                                            Gaps
                                                                                                            19;
                                                       DB 2; Length 1680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium, Plasmodium yoelii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kappe S.H., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.; "A family of chimeric erythrocyte binding proteins of malay
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF031886; AAQ73455.1; -.
SEQUENCE 1680 AA; 197169 MW; 9B955A060B1C67A9 CRC64;
1680 AA; 197169 MW; 9B955A060B1C67A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams J.H.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
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                                                  ch 38.3%; Score 156.5; DB 3
1 Similarity 53.5%; Pred. No. 0.0026;
53; Conservative 9; Mismatches 18
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1263 RKKKAEAAKKAEEKKKAEAAKKAEEEKKKAEAAKKAEEE 1301

Search completed: December 14, 2004, 06:10:19 Job time : 97.5232 secs

49 AEKKEYAA--AEAKYKAEAAKKA----YKAEAAKAAAKE

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5.1.6 Compugen Ltd. GenCore version (c) 1993 - 2004 Copyright

OM protein - protein search, using sw model

December 14, 2004, 05:47:53 ; Search time 95.0717 Seconds (without alignments) 324.499 Million cell updates/sec Run on:

US-10-792-311-6

Perfect score:

1 AKKYAKKEKAYAKKAEKAAK......KKAYKAEAAKAAAKEAAYEA 86 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 23Sep04:* Database :

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2001s:* geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aay82576 Copolymer	Aay82575 Copolymer		4	e	m	Abu44721 Protein e	Abu28559 Protein e	Aar06445 Recombina	Abu40185 Protein e	Abu27824 Protein e	Abu31397 Protein e	Abu47848 Protein e	Abo67048 Klebsiell	Aar06446 Recombina	Aay98499 Peptide #	Aay59044 Amino aci	Aab45852 Nucleic a	Aau04289 Poly-Lys-	Abu38313 Protein e	Abj18771 Pseudomon	Abo80835 Pseudomon	Abu39221 Protein e	Abu50266 Protein e	Aay34055 M. tuberc
SOUTHERIDS	ID	AAY82576	AAY82575	AAY82577	AAY82574	AAY82573	ABU47123	ABU44721	ABU28559	AAR06445	ABU40185	ABU27824	ABU31397	ABU47848	ABO67048	AAR06446	AAY98499	AAY59044	AAB45852	AAU04289	ABU38313	ABJ18771	ABO80835	ABU39221	ABU50266	AAY34055
	DB	3	m	m	m	m	Q	9	9	~	9	9	9	9	7	7	٣	m	4	4	9	v	-	9	9	7
	Length	98	77	109	99	26	407	387	421	154	372	428	323	376	469	106	100	100	100	100	347	347	407	389	388	214
æ	Query Match	100.0	85.9	76.4	65.5	57.0	40.5	40.1	40.1	39.9	39.9	39.4	38.5	38.5	38.5	38.4	38.1	38.1	38.1	38.1	37.7	37.7	37.7	36.2	36.1	35.9
	Score	409	351.5	312.5	268	233	165.5	164	164	163	163	161	157.5	157.5	157.5	157	156	156	156	156	154	154	154	148	147.5	147
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Aay57353 M. tuberc		_	Aab20575 Mycobacte	Abg80418 Haemophil	Abo23507 Haemophil	Abu42038 Protein e	Adf05105 Bacterial	Ada33882 Acinetoba	Ada35034 Acinetoba	Abg71044 Tumour ne	Abul7340 Protein e	Aar84569 Trypanoso	Adq36692 Trypanoso	Aar84565 Trypanoso	Aar84568 Trypanoso	Adq36678 Trypanoso	Aar25206 Synthetic	Aaw30256 Zuotin. 3
AAY57353	ABU36893	ABM67869	AAB20575	ABG80418	AB023507	ABU42038	ADF05105	ADA33882	ADA35034	ABG71044	ABU17340	AAR84569	ADQ36692	AAR84565	AAR84568	ADQ36678	AAR25206	AAW30256
7	o c	v	e	ß	7	9	7	9	9	2	9	7	œ	7	7	œ	7	7
214	214	357	205	372	372	336	361	214	468	80	448	472	507	564	643	717	140	433
6.0	, o	6.5	8.5	4.7	7.1	9.	9.	4.4	2.5	33.9	9.6	33.6	9.6	9.6	33.6	9.6	3.0	9.2
3, 5	, m	ĕ	3,	'n	ň	ň	'n	ň	ň	m	m	m	m	m	m	m	m	m
147	147	147	146.5	142	142	141.5	141.5	140.5	140	138.5	137.5	137.5	137.5	137.5	137.5	137.5	135	133.5
56	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; pashingus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6. AAY82576 standard; peptide; 86 AA. (first entry) 28-JUL-2000 AAY82576

Unidentified.

WO200018794-A1.

06-APR-2000.

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; Gad A,

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

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acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thrombotty, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombotty autoimmune uveoretinitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myroedema, mysathenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease,
                                                                                                                                                                                                                                                                                                                                                                                                                 graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
   the invention are used as molecular weight markers for glatiramer
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Sequence 86 AA;

1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAABAKKKAKAEAKKYAKAKAEKKEYAAABAK 60 Gaps . 0 Length 86; 0; Indels 100.0%; Score 409; DB 3; 100.0%; Pred. No. 6.7e-30; iive 0; Mismatches 0; 98 61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86 YKAEAAKKAYKAEAAKAAAKEAAYEA Query Match Best Local Similarity 100. Matches 86; Conservative 19 ઠે g ઠે 요

RESULT 2

AAY82575 standard; peptide; 77

AAY82575;

(first entry) 28-JUL-2000 Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyrodi, antiinflammatory; antiinflammatory; antiinflammatory; thyromimetic; hamemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified

WO200018794-A1

06-APR-2000.

99WO-US022402. 24-SEP-1999;

98US-0101693P. 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; Gad A, WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

```
AAX AAV82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an coff composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer cactate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases of treated include either cell-mediated or antibody-mediated diseases. Such diseases include either cell-mediated or antibody-mediated diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic ansemia, autoimmune cophoritis, autoimmune thyroidmine uveoretnitis, contact cophoritis, autoimmune thyroidmine, e.g. multiple sclerosis, contact cophoritis, autoimmune thyroidmine, graves disease, disease, disease, disease, disease, disease, disease, disease, disease, idiopathic myxosedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graff disease, properties which are analogous to glatiramer acctate molecules, which copposed properties which are analogous to glatiramer acctate molecules, which
                            Claim 10; Page 14; 72pp; English.
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Sequence 77 AA;

ä 9 9 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAABAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 9; Gaps Score 351.5; DB 3; Length 77; Pred. No. 9.4e-25; 0; Mismatches 0; Indels 9 Query Match
Best Local Similarity 89.5%;
Matches 77; Conservative (셤

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86 77 61 -----YKAEAAKAAAKEAAYEA 61 YKAEAAKKAYKAEAAKAAAKEAAYEA ð 셤

RESULT 3

AAY82577 standard; peptide; 109 AA

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.

glatiramer acetate, autoimmune disease, antiarthritic, neuroprotective; sosteopathic; immunosupressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; antianmaemicy; condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Copolymer; molecular weight marker; TV-marker; immune disease; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified.

NO200018794-A1.

06-APR-2000.

99WO-US022402 24-SEP-1999; 98US-0101693P. 25-SEP-1998;

(YEDA) YEDA RES & DEV CO LTD

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides (I) for determining the molecular weight invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glattramer accetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases of treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, crohn's disease, chronic immune thyroiditis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thrombocytopaenia purpura, colitis, contact cophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, disease, idiopathic mysocedema, myashmina gravis, contact sensitivity disease, disease, idiopathic mysocedema, myashmina gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The properties which are analogous to glatiramer accetate molecules, which cross as molecular weight markers
                                                                                                                                                          Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                                                                                                           Claim 10; Page 14; 72pp; English.
(TEVA-) TEVA PHARM USA INC
                                                                                                          WPI; 2000-317499/27
                                                        Lis D;
                                                     Gad A,
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Sequence 109 AA;

36 1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60 1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKA-----Gaps 27; 76.4%; Score 312.5; DB 3; Length 109; 72.1%; Pred. No. 4.6e-21; ive 1; Mismatches 3; Indels 27 37 -KAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAAKEAAYEA 80; Conservative Query Match Best Local Similarity g ઠે 셤 ઠે

RESULT

9 49

> AAY82574 standard; peptide; 66 AA. AAY82574; AAY82574
> IID AAY
> XX AC AAY
> XX AC AAY
> XX XX COD
> DE COD
> DE COD
> XX XX COD
> XX XX COD
> XX XX COD
> XX XX A ALL
> XX WOO

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.

osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipaoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. acetate; autoimmune disease; antiarthritic; neuroprotective; molecular weight marker; TV-marker; immune disease; glatiramer Copolymer;

Unidentified

WO200018794-A1

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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight to invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an extra composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer cactate related tetrapolymers. The polypeptides may also be used for actated and preventing immune diseases in a mammal. Autoimmune diseases of treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating composities, osteoarthritis, autoimmune haemolytic ansemia, autoimmune cophoritis, autoimmune thyroidmune haemolytic ansemia, autoimmune cophoritis, autoimmune thyroidmune haemolytic ansemia, autoimmune cophoritis, autoimmune thyroidmune wiserenitis, contact sensitivity disease, disease, disease, idiopathic mysocedema, mysethenia gravis, contact cophoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, choryenties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                                                              Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKABEAKKKAKAKAEAKKYAKAAKAEKKEYAAAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.5%; Score 268; DB 3; Length 66 75.6%; Pred. No. 2.9e-17; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 -----YKAEAAKAAKEAYEA
                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 14; 72pp; English.
                                                                                                                                              (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                              99WO-US022402.
                                                                                                    98US-0101693P.
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Best Local Similarity 75.6
Matches 65; Conservative
                                                                                                                                                                                                                                                      WPI; 2000-317499/27
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                                                              24-SEP-1999;
                                                                                                      25-SEP-1998;
                    06-APR-2000.
                                                                                                                                                                                                              Gad A,
셤
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glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3. Copolymer; molecular weight marker; TV-marker; immune disease; 28-JUL-2000 (first entry)

AAY82573 standard; peptide; 56 AA.

RESULT 5 AAY82573

AAY82573;

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer actates treated include at the polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases contributed treated include atther cell-mediated or antibody-mediated diseases Such diseases include atthritic conditions, demyelinating classes and inflammatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, control disease, chronic immune thyroidmine haemolytic ansemia, autoimmune copporative, autoimmune thyroidmine parpura, colitis, contact sensitivity disease, disease, idiopathic mysocedema, mysathenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, chromic manner and delayed-type hypersemalitivity. The collate which are analogous to glatiramer acetate molecules, which come contact molecules which makes them ideal for use as molecular weight markers
diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                (YEDA ) YEDA RES & DEV CO LTD (TEVA-) TEVA PHARM USA INC.
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62.8%;
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Best Local Similarity
Matches 54; Conserv
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                                                                                                                                                  WO200018794-A1
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                                                                                                           Unidentified
                                                                                                                                                                                                                                   24-SEP-1999;
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tp.wipo.int/pub/published_pct_sequences
                                                                                                                                                           Query Match
Best Local Similarity 51.99
Matches 55; Conservative
                                                                                                                                                       Sequence 407 AA;
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                                                                                                                                                             ABU47123 standard; protein; 407 AA.
                                                                                                                                                                       (first entry)
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Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                             Ohlsen KL,
Forsyth RA,
Protein encoded by Prokaryotic essential gene #32650
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                             Malone C,
Carr GJ,
                                                                                                                                                                                                                                            21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                                                                                                                                                                                                                                                       08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                      21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                     (ELIT-) ELITRA PHARM INC.
                                                                                  Salmomella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                           Zamudio C,
Trawick JD,
                                                                                                                      WO200277183-A2
                                                                                                                                                                03-OCT-2002
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Wall D,
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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

2003-029926/02 N-PSDB; ACA50993 Claim 25; SEQ ID NO 75047; 1766pp; English.

the nucleic acid inhibits proliferation of a cell. Also included are:

the 6213 antisense sequences given in the specification where expression

of the nucleic acid inhibits proliferation of a cell. Also included are:

(I) a vector comprising a promoter operably linked to the nucleic acid

encoding a polypeptide whose expression is inhibited by the antisense

concing a polypeptide whose expression is inhibited by the antisense

concing a polypeptide of a host cell containing the vector; (3) an isolated

configuration or its fragment whose expression is inhibited by the

antisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

configuration; (7) identifying a compound that influences the activity of

the gene product or that has an activity against a biological pathway

configured for proliferation, or that inhibits cellular proliferation; (8)

identifying a gene required for cellular proliferation or the biological

configuration which a proliferation-required gene or its gene product lies

correctly agene required for cellular proliferation of an

congound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in strains are strains as present in a culture or collection of

configuration of an organism. The antisense nucleic acids required

for cellular proliferation to isolate candidate molecules for rational

configuration or an organism of an organism of a configuration of an organism of a cellular proliferation or a collection of an organism or a collection of an organism of an organism of a K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at The invention relates to an isolated nucleic acid comprising any

21; Gaps Length 407; Indels 40.5%; Score 165.5; DB 6 51.9%; Pred. No. 3.8e-07; iive 14; Mismatches 16

9

2 1 AKKYAKKEKAYAKKAEKAA----KKAEAKAYK-AAEAKKKAKAEAKKYA----KAAKAEK

19-JUN-2003

ABU47123;

RESULT 6
ABU47123
ID ABU4
XX
AC ABU4
XX
DT 19-J

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the folla antisense sequences given in the specification where expression of the folla antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated can insense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular concerns the activity of the gene product or that has an activity against a biological pathway concerns or that has an activity against a biological pathway or the proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of compound; or (13) identifying the target of a compound that inhibits the extent or product is overexpressed or underexpressed; (12) determining the extent or product is overexpressed or underexpressed; (12) determining the extent or proliferation of an organism. The antisense nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids required for encounted and drawn provers and determination or an organism of an organism contains and antisense nucleic acids are useful for an all an antisense and additional activity are activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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                                       : |||:|| ||||| |||| || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 ||
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Yamamoto R, Forsyth RA,
KEYAAAEAKYKAEA------AKKAYKAEAAKAAA---KEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein encoded by Prokaryotic essential gene #30248.
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                                                                                                                                                                                                                                                               ABU44721 standard; protein; 387 AA
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Carr GJ,
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25-OCT-2001; 2001US-0342923P.
PEBS-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Trawick JD,
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N-PSDB; ACA48591.
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8)
                                                                                                                                                           5
                                                                                                                                                                                                                  the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                            1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-AAEAKKKAKAEAKKYA----KAAKAEKKEYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zyskind JW;
Xu HH;
                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                           16;
                                                                                                                           Length 387;
                                                                                                                         40.1%; Score 164; DB 6; Length 38 llarity 57.0%; Pred. No. 4.9e-07; Conservative 7; Mismatches 17; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein encoded by Prokaryotic essential gene #14086.
                                                                                                                                                                                                                                                                                                   198 aagakkkagabaraaadakkkadagaakaag 230
                                                                                                                                                                                                                                                                 56 AAEAKYKAEA-----AKKAYKAEAAKAAAK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck R,
Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                                                          ABU28559 standard; protein; 421 AA
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Carr GJ,
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25-OCT-2001; 2001US-0342923P.
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2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zamudio C,
Trawick JD,
                                                                                                                  Query Match
Best Local Similarity
Matches 53; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ACA32429
                                                                                          Sequence 387 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001;
06-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                             ABU28559;
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Wall D,
                                                                                                                                                                                                                                                                                                                                                                            ABU28559
                                                                                                                                                                                                                                                                                                                                                          RESULT
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NOV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-collustry of beta-collustry plasmids encode fusion proteins consisting of beta-collustry by the cours between the Protein A and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences, originating from the following protein. The COP-1 polypeptide may be cleaved incoding the following segments: YKK, BAE, KAK, AAK, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the terminal alanine residue is left behind following cNBr cleavage of the cusion protein. The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain amino acids. See also AAQ05665. (Updated on 25-MAR-2003 to correct PA field.)

8\$3888888888888888888888

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identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) prolifing a compound's activity; (11) a culture comprising strains in which the gene or product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for identifying proteins or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids candidated for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence data for this the target prokaryotic essential genes. Note: The sequence data for this contraction of the printed specification, but was obtained the carget of the printed specification, but was obtained to the present sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 KEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAA------KAEKKEYAAAEA
                                                                                                                                                                                                                                                                                                                                                                                                                          18; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                     40.1%; Score 164; DB 6; Length 421; 59.3%; Pred. No. 5.4e-07; ive 7; Mismatches 18; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant copolymer 1-77, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                              in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 RKKAATEAAEKA-KAEAEKKAAAEKA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 KYKA--EAAKKAYKAEAAKAAAKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR06445 standard; protein; 154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 59.3.
Best Local Similarity 59.3.
Conservative 51; Conservative
                                                                                                                                                                                                                                                                                                                                                       Sequence 421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
03-JAN-1991
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Claim 25; SEQ ID NO 68109; 1766pp; English WPI; 2003-029926/02. N-PSDB; ACA44055 Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity. To improve the expression of rCOP-1 polypeptides in E. coli, genes codin for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-Disclosure; Fig 11; 25pp; English.

90EP-00301700 89US-00312541 90US-00473845

16-FEB-1990; 17-FEB-1989; 07-FEB-1990; (REPK) REPLIGEN CORP.

WPI; 1990-255848/34.

Cook KS;

N-PSDB; AAQ05664

Producing

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                                                                                                               78
                                                                                       71
                                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                              41 ---KKYAKAAKAEKKEYAAAEAKYKAEA--------AKKAYKAEAAKAA--
                                                                  2 KKYAK-KEKAYAKKAEKA-AKKAEAKAY-KAAEAKKKAKAEA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zyskind JW;
Xu HH;
                                            Gaps
                                            46;
                     Length 154;
                                            20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #25712
                    Score 163; DB 2;
Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto R,
                    Query Match
39.9%; Score 163; DB
Best Local Similarity 42.3%; Pred. No. 2.3e
Matches 55; Conservative 9; Mismatches
                                                                                                                                                                                                                                          ABU40185 standard; protein; 372 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
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                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELITRA PHARM INC.
                                                                                                                                                                                  132 AEKAKEAEYK 141
                                                                                                                                                             79 --- AKEAAYE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                            Pseudomonas putida
Sequence 154 AA
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Wall D,
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                                                                                                                                                                                                                      RESULT 10
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid concerned are concerned acid; (2) a host cell containing the vector; (3) an isolated concerned acid; (4) an antibody capable of specifically binding the polypeptide by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide of specifically binding the polypeptide of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway required for proliferation, or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sectivity; (11) a culture comprising strains in which the gene organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sectivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent convoluter acids required for proliferation of an organism. The antisense nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 372 AA;

148 AKKAAEKQQADIAKKKAEDEAKKKAEEEAKKKAAEEAKKKAAEEAKKKAAEEAKKKAAED 207 1 AKKYAKKEKA--YAKKAE-KAAKKAEAKAYKAA--EAKKKAKAEAKKYA----KAAKA 49 Gaps 12; 39.9%; Score 163; DB 6; Length 372; 53.1%; Pred. No. 5.8e-07; Live 12; Mismatches 22; Indels 1 208 AKKKAAAEDAKKKAAEEAKKKAAADAQKKKAQEAARKA 245 EKKEYAAAEAKYK-AEAAKKAYKAEAAKAAAKEAAYEA 86 Conservative Local Similarity nes 52; Conserv 20 Query Match Best Loc Matches đ 8 ઠે

ABU27824 standard; protein; 428 AA ABU27824; RESULT 11

19-JUN-2003 (first entry)

Protein encoded by Prokaryotic essential gene #13351.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Enterobacter cloacae.

WO200277183-A2

03-OCT-2002.

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342921P. 08-FEB-2002; 2002US-00072881. 06-MAR-2002; 2002US-0362699P.

ELITRA PHARM INC. (ELIT-) Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, Wang L, Wall D,

2003-029926/02 N-PSDB; ACA31694 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 55748; 1766pp; English.

The invention relates to an isolated mucies acts compirising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense conclains a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated caristense nucleic acid; (4) an antibody capable of specifically binding to polypeptide or its fragment whose expression is inhibited by the activity of the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular correct proliferation or the activity of a gene in an operon required for the polypeptide; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for the strains or screening for homologous nucleic acids required for cellular proliferation to solate candidate molecic acids are useful for for cellular proliferation of an organism. The antisense nucleic acids are useful for for cellular proliferation of solate candidate molecic acids are useful for for all the strains is solate candidate molecic acids are useful for for all the strains to screening for homologous nucleic acids required for the strains is solate candidate molecic acids are useful for for all the strains is solate and acids are useful for formal acids and a drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Mult form Mult community at the printed sequences. The invention relates to an isolated nucleic acid comprising any

Sequence 428 AA;

39.4%; Score 161; DB 6; Length 428; 47.5%; Pred. No. 1e-06; le-06; -hes 21; Indels Mismatches 16; Local Similarity 47.5 ses 48; Conservative Query Match Best Loc Matches

1 AKKYAKKEKAYAKKAEKAAKK-----AEAKAYKAAEAKKKAKAEAKKYAKAAKAEKK 52

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186 даараоккаереааккаараоккаереааккааоедекка 226 98 53 EYAAAEAKYKAEAAKKA-----YKAEAAKAAAKEAAYEA ઠે 셤

RESULT 12 ABU31397

ABU31397 standard; protein; 323 AA ABU31397; **EXEXEXEX**

(first entry) 19-JUN-2003

Protein encoded by Prokaryotic essential gene #16924.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                     invention relates to an isolated nucleic acid comprising any one
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                                                                 21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342921P
08-FEB-2002; 2002US-00072881.
06-MAR-2002; 2002US-0362699P.
                                                   21-MAR-2002; 2002WO-US009107
                                                                                                              ELIT-) ELITRA PHARM INC.
      Klebsiella pneumoniae.
                                                                                                                            Zamudio C,
Trawick JD,
                                                                                                                                                  WPI; 2003-029926/02.
N-PSDB; ACA35267.
                    WO200277183-A2.
                                    03-OCT-2002
                                                                                                                             ņ,
                                                                                                                             Wang
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the 6213 antiseness sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gane in an operon required for proliferation or the activity of a gane in an operon required for proliferation or the activity against a biological pathway in equival to that has an activity against a biological pathway in which a proliferation or the biological pathway in which the test compound that inhibits proliferation of an compound, a activity; (11) a culture comprising strains in which the gene or which the test compound that inhibits proliferation of an compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of the strains or (13) identifying the arrange or collection of a strains; or (13) identifying the arrange or acids are useful for acids acids are useful and acids are useful for acids are useful and acids are acids are acids are acids are acids identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginos. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained directly from WIPO at in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences

Sequence 323 AA;

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EKAYAKKAEKAAKKAEAKAYK-AAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAA 66
                                                 3;
38.5%; Score 157.5; DB 6; Length 323; 55.7%; Pred. No. 1.6e-06; Indels 3; ive 11; Mismatches 21; Indels 3;
                                               44; Conservative
                             Best Local Similarity
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      Query Match
                                               Matches
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KKAYKAEAAKAAAKEAAYE 85 22

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113 KKAQQEAAKQAAAEKAAAE 131

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Protein encoded by Prokaryotic essential gene #33375.
                        ABU47848 standard; protein; 376 AA.
                                                                                                                   (first entry)
                                                                                                                      19-JUN-2003
                                                                        ABU47848;
ABU47846
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Antisense; prokaryotic essential gene; cell proliferation; drug design.

Salmomella typhi.

WO200277183-A2.

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

03-OCT-2002.

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0042923P. 08-FEB-2002; 2002US-00572851. 06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

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Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, Wang L, Wall D,

WPI; 2003-029926/02. N-PSDB; ACA51718.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 75772; 1766pp; English.

the 6113 antisease sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisease nucleic acid; (2) a host cell containing the vector; (3) an isolated oplypeptide or its fragment whose expression is inhibited by the antisease antisease nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for the gene product or that has an activity against a biological pathway required for that has an activity against a biological pathway in which a gene required for cellular proliferation or the biological pathway is agne on which the test compound that inhibits spendification of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. arreus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at one of The invention relates to an isolated nucleic acid comprising any

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Search completed: December 14, 2004, 06:01:15
                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ06446.
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                                                                                                                                     Recombinant
                                                                                                                                                                                                              22-AUG-1990.
                                                                                                                                                                                          EP383620-A.
                                                                                                                                                                     Synthetic.
                                                               AAR06446;
                                                                                                                                                                                                                                                                                                           Cook KS;
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                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a new isolated nucleic acid encoding a Klebsiella pheumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                               New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-AAEAKKKAKAEAKKYA----KAAKAEKKEYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 EKAYAKKAEKAAKKAEAKAYK-AAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAA
                                                               Gaps
                                                                                                                                                                                                                                                                                     Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3,
                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.5%; Score 157.5; DB 7; Length 469; 55.7%; Pred. No. 2.3e-06; ive 11; Mismatches 21; Indels 3
                                          Length 376;
                                        38.5%; Score 157.5; DB 6; Length 54.8%; Pred. No. 1.8e-06; ive 10; Mismatches 17; Indels
                                                                                                                                              185 AAEAKKKAEAEAAKAAADAKKKADAEAAKAAAE 217
                                                                                                                                                                                                                                                                Klebsiella pneumoniae polypeptide seqid 13565.
                                                                                                                          56 AAEAKYKAEA-----AKKAYKAEAAKAAAK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 13565; 932pp; English.
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                  ABO67048 standard; protein; 469 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           (GENO-) GENOME THERAPEUTICS CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                        99US-0117747P
                             Query Match
Best Local Similarity 54.00
Best Local Similarity 54.00
Conservative
                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                   Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Osborne M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABD00619
                    Sequence 376 AA;
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for improve the expression of rCOP-1 polypeptides in B. coli, genes coding for rCOP-1-19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 UG4661009, NRL B-15910), a plasmid used to express Protein A. Che resulting plasmids encode fusion proteins consisting of beta-cours between the Protein A, and rCOP-1 sequences. A methionine residue cocurs between the Protein A and rCOP-1 sequences, originating from the core in order that the COP-1 soquences, originating from the fusion protein. rCOP-1-19 contains oligonucleotide duplexes in coding the following segments: YKK, AAE, KAK, EXA, KKA, KEA, ARA, KAR, CAB, ARA REA, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the fusion protein. The product prevents or arrests crawper inchemical and demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain and conference or conference to conference c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 5.3e-07;
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AAR06446 standard; protein; 106 AA
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90US-00473845.
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Best Local Similarity
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Job time : 96.0717 secs

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December 14, 2004, 05:52:22 ; Search time 213.367 Seconds (without alignments) 143.965 Million cell updates/sec
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| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 6, Appli Sequence 5, Appli	۲ 4	'n	Sequence 75047, A Sequence 72645, A	Sequence 56483, A	Sequence 68109, A	Sequence 55748, A	Sequence 59321, A	Sequence 75772, A	Sequence 120, App
SUMMARIES	US-09-816-989A-6 US-09-816-989A-5	US-09-816-989A-7 US-09-816-989A-4	US-09-816-989A-3	US-10-282-122A-75047 US-10-282-122A-72645	US-10-282-122A-56483	US-10-282-122A-68109	US-10-282-122A-55748	US-10-282-122A-59321	US-10-282-122A-75772	US-10-127-032-120
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Sequence 66237, A	Sequence 67145, A	Seguence 78190, A							Sequence 45264, A		Sequence 36, Appl	Seguence 10710, A			Sequence 5, Appli		Sequence 201, App	Sequence 52, Appl	Sequence 60257, A	Sequence 3, Appli	Sequence 9889, Ap	Sequence 2, Appli	Sequence 197135,	Sequence 37076, A	Sequence 10221, A	Seguence 45755, A		Sequence 193381,	Sequence 2, Appli	5, 3	Sequence 27, Appl
US-10-282-122A-66237	US-10-282-122A-67145	US-10-282-122A-78190	US-10-229-567-27	US-10-282-122A-62547	US-10-282-122A-64817	US-09-820-843A-8	US-10-467-421-16	US-10-282-122A-69962	US-10-282-122A-45264	US-10-726-692-50	US-10-726-692-36	US-10-739-930-10710	US-10-390-472-2	US-10-282-122A-67699	US-10-184-832-5	US-10-282-122A-61735	US-10-051-643-201	US-10-205-979-52	US-10-282-122A-60257	US-10-229-567-3	US-10-156-761-9889	US-09-816-989A-2	US-10-425-115-197135	US-10-425-114-37076	US-10-156-761-10221	US-10-767-701-45755	US-10-437-963-152005	US-10-437-963-193381	US-10-262-209-2	US-10-240-430-5	US-09-820-843A-27
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347	389	388	214	214	214	372	372	336	448	507	717	272	433	329	452	212	223	223	139	222	376	45	568	636	217	281	827	926	130	130	356
37.7	36.2	36.1	35.9	35.9	35.9	34.7	34.7	34.6	33.6	33.6	33.6	33.0	32.6	32.3	32.0	31.9	31.7	31.7	31.1	31.1	31.1	30.9	30.9	30.9	30.6	30.4	30.3	30.2	30.1	30.1	30.1
154	148	147.5	147	147	147	142	142	141.5	137.5	137.5	137.5	135	133.5	132	131	130.5	129.5	129.5	127	127	127	126.5	126.5	126.5	125	124.5	124	123.5	123	123	123
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ALIGNMENTS

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Sequence 6, Application US/09816989A
; Sequence 6, Application US/09816989A
; Patent No. US20020115103A1
; GENERAL INFORMATION:
APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doria
APPLICANT: Lis, Doria
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; TITLE OF INVENTION: UNMBER: US/09/816,989A
; CURRENT APPLICATION NUMBER: 60/101,693
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR PILING DATE: 1998-09-25
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENTH: 86
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100.0%; Pred. No. 4.3e-28;
tive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Matches 86; Conservative
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816, 989A
CURRENT FILING DATE: 2001-03.23
PRIOR PILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101, 693
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE PATENTION OF SEQ ID NOS: 7
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                       1 AKKYAKKAEKAYAKKAKAKAKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
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Best Local Similarity 75.6%; Pred. No. 3.9e-16;
Matches 65; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                     Sequence 4, Application US/09816989A Patent No. US20020115103A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gad, Alexander
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                      US-09-816-989A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-816-989A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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                                                                                                                                                                                                                                                                  ATTLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REFERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT FILING DATE: 2001-03-23 PRIOR PILING DATE: 1998-09-25 PRIOR PLILING DATE: 1998-09-25 PRIOR PILING DATE: 1999-09-24 NUMBER OF SEQ ID NOS: 7 SOFTWARE: PORTOR PILING DATE: 1999-09-34 SOFTWARE: PARCHIN VERSION 3.1 SEQ ID NOS: 7 LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: COPOLYMER 1 VELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
CURRENT APPLICATION NUMBER: US/0816, 989A
CURRENT FILING DATE: 1090-09-25
PRIOR APPLICATION NUMBER: 60/101, 693
PRIOR PILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ņ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
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Pred. No. 1e-19;
1; Mismatches 3; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9; Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 351.5; DB 9
Pred. No. 3.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YKAEAAKAAAKEAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
61 YKAEAAKKAYKAEAAKAAAKEAAYEA
                                                                                                                                  ; Sequence 5, Application US/09816989A, Patent No. US20020115103A1, GENERAL INFORMATION: APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 7, Application US/09816989A; Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.9%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 89.5 Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 72.1
Matches 80; Conservative
                                                                                 RESULT 2
US-09-816-989A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-816-989A-5
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US-09-816-989A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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1 AKKYAKK-EKAYAKKA-----EKAAKKAEAKAYKAAEAKKKA---

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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-AAEAKKKAKAKAEAKKYA----KAAKAEKKEYA 55
     183 AK-AAADAKKKAEAEAAKAAAEAKKKAEAEAAKAAAEAKKKADAEA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 AAEAKKKAEAEAAKAAADAKKKADAEAAKAAAE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 AAEAKYKAEA-----AKKAYKAEAAKAAAK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Salmonella paratyphi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 72645
LENGTH: 387
                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                   Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
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Best Local Similarity 57.0<sup>§</sup>
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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                                                          30;
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57.0%; Score 233; DB 9; Length 56; ilarity 62.8%; Pred. No. 3.2e-13; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                           1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAK--
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14; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                           -----YKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                   61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 75047, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Salmonella typhimurium
US-10-282-122A-75047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Tawick, John
APPLICANT: Tawick, John
APPLICANT: Tawick, John
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 KEYAAAEAKYKAEA---
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Best Local Similarity
                              Local Similarity
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LENGTH: 407
  Query Match
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Matches
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FILE REPERENCE: ELITICATION OF ESSENCIAL GENES IN ALCOORGANISMS
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-23
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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57.0%; Pred. No. 2e-06;
ive 7; Mismatches 17; Indels 16; Gaps
US-10-282-122A-72645
; Sequence 72645, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (78)...(78)
OTHER INFORMATION: X=any amino acid FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MISC_FEATURE

DOCATION: (303)...(303)

CTHER INFORMATION: X=any amino acid

US-10-282-122A-72645
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APPLICANY: AU, H.,

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PLILING DATE: 2000-05-23

PRIOR PLILING DATE: 2000-05-26

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-09

PRIOR PLILING DATE: 2000-10-23

PRIOR PLILING DATE: 2000-11-27

PRIOR PLILING DATE: 2001-10-29

PRIOR PLILING DATE: 2001-02-09

PRIOR PLILING PLILING DATE: 2001-02-09

PRIOR PLILING PLILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKA--YAKKAE-KAAKKAEAKAYKAA--EAKKKAKAEAKKYA-----KAAKA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 372;

Best Local Similarity 53.1%; Pred. No. 2.3e-06;

Matches 52; Conservative 12; Mismatches 22; Indels 12; Gaps
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| Publication No. US20040029129A1
| GENERAL INFORMATION:
| APPLICANT: Mangeu
| APPLICANT: Malone, Cheryl
| APPLICANT: Haselbeck, Robert
| APPLICANT: Wall, Daniel
| APPLICANT: Trawick, John
| APPLICANT: Trawick, John
| APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1 SEQ ID NO 68109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Pseudomonas putida
US-10-282-122A-68109
Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                       Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Forsyth, R.
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PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-03-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-11-27

PRIOR PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PRIOR DATE: 2000-11-27

PRIOR PRIOR DATE: 2000-11-27

PRIOR PRILING DATE: 2000-11-27

PRIOR PRILING DATE: 2000-11-27

PRIOR PRILING DATE: 2001-02-09

PRIOR PRILING DATE: 2001-02-09
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 40.1%; Score 164; DB 15; Length 421; Local Similarity 59.3%; Pred. No. 2.2e-06; nes 51; Conservative 7; Mismatches 18; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PUDLICATION NO. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                     ; Sequence 56483, Application US/10282122A; Publication No. US20040029129A1; GENERAL INFORMATION:
                                                                                                                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Wall, Daniel
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Best Local S
Matches 51
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APPLICANT: Yayarina Juditah
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yangamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
TILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/220
PRIOR PILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/2030,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PRIOR APPLICATION NUMBER: 60/23,625
PRIOR PELING DATE: 2000-112-22
PRIOR PELING DATE: 2001-12-22
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-04
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 201-03-16
PRIOR FILING D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.5%; Score 157.5; DB 15; Length
55.7%; Pred. No. 5.9e-06;
tive 11; Mismatches 21; Indels
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    APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 KKAQQEAAKQAAAEKAAAE 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-282-122A-59321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Zyskind, Judith
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APPLICANT: FORSYTH, R.
APPLICANT: FORSYTH, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-03-220
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-65
PRIOR FILING DATE: 2000-09-06
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                          CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2001-02-09
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    APPLICATION NUMBER: US/10/282,122A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Enterobacter cloacae US-10-282-122A-55748
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
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SEQ ID NO 55748
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Yamamoto, Robert
Forsyth, R.
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APPLICANT:
APPLICANT:
APPLICANT:
CURRENT
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APPLICANT: XU, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-36
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-06
PRIOR DATE: 2001-
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Best Local Similarity 47.6%; Pred. No. 1.3e-05;
Matches 49; Conservative 11; Mismatches 21;
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Chery1
APPLICANT: Malone, Chery1
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Zyskind, Undith
APPLICANT: Wall, Daniel
APPLICANT: Tawkick, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                               Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Publication No. US20030113742A1

SEQUENCEAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Whiteley, Marvin
APPLICANT: Bangera, M. Gita
APPLICANT: Lory, Stephen
APPLICANT: Lory, Stephen
APPLICANT: Genemberg, Everett Peter
ITILE OF INVENTION: BIOFILM FORMATION
FILE OF INVENTION: BIOFILM FORMATION
FILE OF INVENTION: BIOFILM FORMATION
CURRENT APPLICATION NUMBER: US 60/285,190
FRIOR APPLICATION NUMBER: US 60/285,190
FRIOR APPLICATION NUMBER: US 60/344,142
FRIOR APPLICATION NUMBER: US 60/344,142
FRIOR FILING DATE: 2001-04-20
FRIOR FILING DATE: 2001-04-20
FRIOR FILING DATE: 2001-04-20
SOFTWARE FASTEEQ for Windows Version 4.0
SEQ ID NO 120
LENGTH: 347
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                       Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTYARE: Patentin version 3.1 SEQ ID NO 75772 LENGTH: 376
                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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                                                                                                                                                                                                                                                                                                                                                                          Length 376;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Indels
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                                                                                                                                                                                                                                                                                                                                                                      38.5%; Score 157.5; DB 15; 54.8%; Pred. No. 7e-06; tive 10; Mismatches 17; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 AAEAKKKAEAEAAKAAADAKKKADAEAAKAAAE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 AAEAKYKAEA-----AKKAYKAEAAKAAAK 80
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 54.8#
Matches 51; Conservative
                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Salmonella typhi
US-10-282-122A-75772
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US-10-282-122A-66237
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US-10-127-032-120
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Matches

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Indels 22; Gaps

Length 347;

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| CURRENT FILING DATE: 2003-02-20
| PRIOR APPLICATION NUMBER: 60/191,078
| PRIOR PELICATION NUMBER: 60/191,078
| PRIOR FILING DATE: 2000-03-21
| PRIOR FILING DATE: 2000-05-23
| PRIOR FILING DATE: 2000-05-23
| PRIOR FILING DATE: 2000-05-26
| PRIOR FILING DATE: 2000-05-26
| PRIOR FILING DATE: 2000-05-06
| PRIOR FILING DATE: 2000-09-06
| PRIOR FILING DATE: 2000-09-06
| PRIOR FILING DATE: 2000-10-23
| PRIOR PLICATION NUMBER: 60/23,625
| PRIOR FILING DATE: 2000-11-27
| PRIOR PLICATION NUMBER: 60/25,931
| PRIOR FILING DATE: 2001-12-22
| PRIOR PLICATION NUMBER: 60/26,366
| PRIOR FILING DATE: 2001-02-16
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2 KKYAKKEKAYAKKAEKAAK-KAEAKAYKAA-----EAKKKAKAEAKKYAKAAKAE-- 50

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Search completed: December 14, 2004, 06:59:42 Job time: 214.367 secs

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TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 7, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 13565, A
Sequence 64, Appl
Sequence 251, Appl
Sequence 27, Appl
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                                                                                December 14, 2004, 05:47:53 ; Search time 24.1308 Seconds (without alignments) 236.351 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
            version 5.1.6
- 2004 Compugen Ltd.
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US-08-405-743A-7
US-08-405-743A-7
US-08-405-743A-7
US-08-167-644
US-08-167-644
US-08-167-644
US-09-252-991A-29581
US-09-252-991A-29581
US-09-328-352-6321
US-09-328-352-6321
US-09-318-352-6321
US-09-318-352-6321
US-09-318-346-8
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US-08-316-894-8
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US-09-205-426-201
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Maximum Match 100%
Listing first 45 summaries
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            GenCore (c) 1993
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seq length: 200000000
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Match Length DB
                                                                                                                                US-10-792-311-6
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US-09-405-743A-5
US-09-405-743A-5
; Sequence 5, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REPREENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09/405,743A
; CURRENT PILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
LEMOTH: 77
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Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yead Research and Development Co., Ltd.
APPLICANT: Yead Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DESCRIPTION OF Artificial Sequence:
OTHER INFORMATION: PEPTIDE
US-09-405-743A-6
                    US-09-041-889-3
US-08-041-889-3
US-09-041-889-3
US-09-041-889-40
US-09-041-889-40
US-09-041-889-40
US-09-041-889-32
US-09-270-767-39148
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US-09-041-889-32
US-09-041-889-34
US-09-041-889-4
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             -09-489-039A-13743
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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REPERBINGE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 66
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TITLE OF INVENTION: G1207.A
TILLE REFERENCE: 60807.A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT APPLICATION DATE: 1999-09-24
NUMBER OF SEQ 1D NOS: SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.4%; Score 312.5; DB 4; Length 109; 72.1%; Pred. No. 3e-22; Live 1; Mismatches 3; Indels 27
                                                                                                      Score 351.5; DB 4; Length 77; Pred. No. 5.4e-26; 0; Mismatches 0; Indels
                   OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: PEPTIDE
US-09-405-743A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/09405743A; Patent No. 6514938; GENERAL INFORMATION:
                                                                                                        Query Match
Best Local Similarity 89.5%;
Matches 77; Conservative
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Best Local Similarity
Matches 80; Conserval
                                                              US-09-405-743A-5
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US-09-405-743A-7
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US-09-405-743A-4
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SEQ ID NO 7
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US-09-489-039A-13565

Sequence 13565, Application US/09489039A

Sequence 13565, Application US/09489039A

Sequence 13656, Application US/09489039A

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT PILING DATE: 1999-01-29

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13565

LENGTH: 469
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                                                Gaps
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APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION UNBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
Score 268; DB 4; Length 66; Pred. No. 2.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 57.0%; Score 233; DB 4; Length 56 Best Local Similarity 62.8%; Pred. No. 3.3e-15; Matches 54; Conservative 2; Mismatches 0; Indels
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                                              Indels
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OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: PEPTIDE
US-09-405-743A-3
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1 Similarity 55.7%; Pred. No. 2.8e-07;
44; Conservative 11; Mismatches 21;
                                            0; Mismatches
                                                                                                                                                                                                                   50 -----YKABAAKAAKBAYBA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 -----YKABAKAAKEAAYEA 56
                                                                                                                                                                           61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09405743A Patent No. 6514938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Klebsiella pneumoniae
Query Match
Best Local Similarity 75.6%;
Matches 65; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-489-039A-13565
                                                                                                                                                                                                                                                                            RESULT 5
US-09-405-743A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PE
SEQ ID NO 3
LENGTH: 56
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STATE: California
COUNTRY: U.S.A.
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                                                                                                               US-08-167-641C-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-08-460-890A-64
; Sequence 64, Application US/08460890A
; Patent No. 5994109
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: MITHODS OF USE
NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-460-890A-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Sulce 4 700
CITY: Los Angeles
STATE: California
COUNTY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastESEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: Une 5, 1995
CLASSIFICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/066
TELECOMMUNICATION INFORMATION:
MELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                     ||| : | :|||:|| |
263 KKAQQEAAKQAAAEKAAAE 281
                                            67 KKAYKAEAAKAAAKEAAYE 85
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TELEFAX: (213) 955-0440
TELEX: 67-1510
INFORMATION FOR SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
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1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
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Sequence 64, Application US/08167641C

Patent No. 6033884

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSED: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 5410 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 100;
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US-08-167-641C-64
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55.3%; Pred. No. 7.7e-08;
tive 6; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT ITE: SUCISED COPERATING SYSTEM: IBM COMPACIBLE COPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FASTENG for Windows 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C FILING DATE: December 14, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/0893/02725
APPLICATION NUMBER: PCT/0893/02725
APPLICATION NUMBER: PCT/0893/02725
ATTONNEY/AGENT INFORMATION:
NAME: WASDING RICHARD CONTRACT OF THE CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || ||:| || || AKAKAKAKAKAKAKA 86
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 amino acids
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Best Local Similarity 55.3
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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RESULT

59 AKYKAEAAKKAYKAEAAKAAAKEAA 83

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APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gritchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES:
ADDRESSEE: Lyon & Lyon
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 38.1%; Score 156; DB 3; Length 100; 1 Similarity 55.3%; Pred. No. 7.7e-08; 47; Conservative 6; Mismatches 30; Indels
                                                                                                                                                  APPLICANT: Which its and its a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: CAILLULAGE
COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Fast-SEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,971A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRICA TOWN NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
ATTORNEY AGENT INFORMATION:
NAME: Warbhard JI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 312/063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-040
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 AKAKAKAKAKAKAKAKAKAKA 86
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                                       Sequence 64, Application US/08460971A
Patent No. 6150168
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 100 amino acids
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STRANDEDNESS: single
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MOLECULE TYPE: peptide
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Best Local Similarity
US-08-460-971A-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
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Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 38.1%; Score 156; DB 3; Length 100; Best Local Similarity 55.3%; Pred. No. 7.7e-08; Matches 47; Conservative 6; Mismatches 30; Indels
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOCTAMAE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 20, 1993
ATOMEN'S WARTON:
NAME: WARDURY, RICHAR'D
REGISTRATION NUMBER: 32,32,32
ATOMENEY AGENT INFORMATION:
NAME: WARDURY, RICHAR'D
REGISTRATION NUMBER: 32,32,32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "18-09-252-991A-29581

Sequence 29581, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 AKYKAEAAKKAYKAEAAKAAKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 AKAKAKAKAKAKAKAKAKAKA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212/078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 212/(
TELECOMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELERX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 anino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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; Sequence 64, Application US/08462040; Patent No. 6177554

RESULT 10 US-08-462-040-64

Length 214;

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US-09-417-264-27
                                        Query Match
                                                              Best Loc
Matches
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Patent No. 6033864

GENERAL INFORMATION:

BAPLICANT: Braun, Jonathan

APPLICANT: Cohary, Offer

TITLE OF INVENTION: Diagnosis, Prevention and Treatment of

TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using

TITLE OF INVENTION: Microbial UC pANCA antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                      44
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FILE REFERENCE: 107196.136
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT PELLING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-0-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29581
                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                     DB 4; Length 407;
                                                                                                                                                                                                                                                                                                                                                                         21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 KKKAAEEAKKKAAAEAAKKKAAVEAAKK--KAAAAAAAARKAA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 --KAAKAEKKEYAAAEAKYKA--EAAKKAYKAEAAKAAAKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                     Score 154; DB 4
Pred. No. 5e-07;
                                                                                                                                                                                                                                                                                                                                                                         11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                   37.78;
                                                                                                                                                                                                                                                                                                                                                                         49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-09-041-889-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  San Diego
: California
RY: USA
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                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                            US-09-252-991A-29581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-09-041-889-27
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GENERAL INFORMATION:

APPLICANT: Braun, Jonathan
APPLICANT: Chavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LiP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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 ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||
                                                                                                                                                                                                                                                                                             111 AKKVAK--KAPAKKATKAAKKAATKAPARKAATKAPAKKAATKAPAKKAVKATKSPAKKV 168
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                                                                                                        34; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
Match 35.9%; Score 147; DB 3; Local Similarity 50.0%; Pred. No. 1.1e-06; les 47; Conservative 3; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 147; DB 4;
Pred. No. 1.1e-06;
3; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 TKAVKKTAVKASVRKAATKAPAKKAAAKRPATKA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 TKAVKKTAVKASVRKAATKAPAKKAAAKRPATKA 202
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REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 09/041,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/09/417,264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/09417264 Patent No. 6537768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.9%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.9
Best Local Similarity 50.0
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-417-264-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 4370 no CITY: San Diego STATE: California
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US-09-543-681A-5390

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Sequence 5390, Application US/09543681A
Patent No. 6605709
GRNERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-1002-001
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5390
LENGTH: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5169, Application US/09328352

Patent No. 6562958

GENERAL INPORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5169
LENGTH: 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AKKEKAYAKKAEKAAKKAEAK----AYKAAEAKKKAKAEAKKYAKAA---KAEK-KEYAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEK--AYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAK--AEKKEYA- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 34.6%; Score 141.5; DB 4; Length 361; Best Local Similarity 52.1%; Pred. No. 6.3e-06; Matches 50; Conservative 12; Mismatches 19; Indels 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 34.4%; Score 140.5; DB 4; Length 214; Best Local Similarity 51.0%; Pred. No. 4.5e-06; Matches 50; Conservative 10; Mismatches 23; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Indels
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87 ADKKAAEAKRQAEADKKAABAKRKAEAEKKAE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 ----AAEAKYKAEAAKKA----YKAEAAKAAAKEAAYE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 AEAKAKAEADAKA-KAEADAKAKAAAEAKAKAAAEA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 AEAKYKAEAAKKAYKAEA---AKAAAK---EAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: December 14, 2004, 05:50:18 Job time: 24.2737 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Proteus mirabilis US-09-543-681A-5390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-328-352-5169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-328-352-5169
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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 14, 2004, 05:47:53 ; Search time 25.0654 Seconds (without alignments) 418.411 Million cell updates/sec Run on:

US-10-792-311-7 519 1 AKKYAKKABKAYAKKAKAAAK......AKAYKAEAAKAAAKEAAYEA 109 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters: 283416 seqs, 96216763 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	189.5	36.5	421	7	JV0057	tolA protein - Esc
7	181.5	35.0	394	N	F90725	Пį
٣	181.5	35.0	394	~	G85576	membrane spanning
4	181	34.9	210	~	A25550	histone H1 - sea u
Ŋ	179		347	~	E83525	in
9	178		376	~	AG0592	protein
7	178		388	~	AC0138	colicin
æ	175.5	33.8	344	~	S34153	u
6	172.5	33.2	211	~	A28100	histone Hī-beta, e
10	171.5	33.0	1390	~	S51364	sperm tail-specifi
11	170.5	32.9	248	Н	HSUR1P	histone H1, gonada
12	170.5	32.9	1701	N	T09127	probable erythrocy
13	165		220	~	A28456	
14	164.5	31.7	231	~	S59589	histone H1 - Chlam
15	164	31.6	265	~	S19113	cgcr-4 protein - C
16	164	31.6	311	~	T17698	hypothetical prote
17	163.5	31.5	384	N	B43592	outer membrane pro
18	163	31.4	182	~	S61926	
19	163	31.4	225	7	B28456	histone H1.11L - c
20	162.5	31.3	1128	7	T30296	R27-2 protein - Tr
21	162	31.2	356	7	A82152	tolA protein VC183
22	161.5		328	7	A44993	cytosolic repetiti
23	191	31.0	219	7	E60110	repetitive protein
24	160.5	30.9	206	٦	HSTR1R	
25	160.5	30.9	226	Н	S51660	
56	159.5	30.7	219	~	C28456	H1.1
27	158	30.4	219	Н	HSHU1B	histone H1-4 [vali
	157	30.3	771	-1	343	caldesmon - ch
29	156.5	30.2	218	~	A23055	histone H1.01 - ch

RESULT 2 F90725

hypothetical prote	histone H1-II - Vo	polyhydroxyalkanoa	conserved hypothet	outer membrane int	histone H1.03 - ch	probable translati	histone H1 - mouse	histone H1-gamma;	histone H1 (clone	histone H1 - musco	histone H1 - mouse	histone H1.1 - Cae	histone H1 - mouse	hypothetical prote	regulatory protein
829309	JN0748	G83013	H71321	G64064	D28456	T11583	A28470	A26721	T06257	801262	149742	T23778	S49482	AE1689	A35630
~	N	~	~	7	7	N	N	N	7	7	~	7	~	7	7
217	241	309	369	372	224	1403	212	217	288	218	219	208	221	243	340
29.8	29.8	29.8	29.6	29.6	29.4	29.1	28.9	28.9	28.9	28.5				28.3	
154.5	154.5	154.5	153.5	153.5	152.5	151	150	150	150	148	147.5	147	147	147	147
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

 RESULT 1 JV0057 tolA protein - Escherichia coli (strain K-12) C;Species: Escherichia coli C;Species: Bacherichia coli C;Species: Bacherichia coli C;Accession: JV0057; B64810 R;Levengood, S.K.; Webster, R.E. J. Bacteriol 171, 6600-6609, 1989 A. Hateriol 171, 6600-6609, 1989
 A; Reference number: JV0057; MUID:90078104; PMID:2687247 A; Reference number: JV0057; MUID:90078104; PMID:2687247 A; Recession: JV0057 A; Recent type: DNA A; Residuacs: 1-421 cLEV A; Residuacs: 1-421 cLEV A; Residuacs: UNIPROT: P19934; GB:M28232; NID:g148018; PIDN:AAA24683.1; PID:g148019
 A; Experimental source: strain JM105 A; Note: the authors translated the initiation codon GTG for residue 1 as Val A; Note: the authors translated the initiation codon GTG for residue 1 as Val R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col A; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: B64810 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-421 <blat></blat>
 A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960; A;Experimental source: strain K-12, substrain MG1655 C;Comment: tolA and tolB proteins are necessary for colicins E2, B3, A, and K to reach the C;Genetics: A;Gene: tolA A;Apa position: 17 min A;Astart codon: GTG
 C; Keywords: nucleotide binding; P-loop; transmembrane protein F;14-34/Domain: transmembrane #status predicted <mss> F;78-301/Domain: helical #status predicted <hsr> F;355-362/Region: nucleotide-binding motif A (P-loop)</hsr></mss>
 Query Match 36.5%; Score 189.5; DB 2; Length 421; Best Local Similarity 53.0%; Pred. No. 1.7e-05; Matches 61; Conservative 11; Mismatches 32; Indels 11; Gaps 5;
Qy 1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAEBAKKKAKAEAKKYAK-EAAK 55 :: :
Qy 56 AKKBAY-KAEAKKYAKAAKAEKKEYAABEAKKAEAAKAYKAEAAKAAAKBA 106

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Reference number: A25550; MUID:87040778; PMID:3022245
                                                                                                                                                                                                                              34.9%;
50.0%;
                                                                                                                                                                                                                                                                                  58; Conservative
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Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <STO>
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-376 < PAR>
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A,Gene: tolA, PA0971
                                                                                                                                                                                                                                 Query Match
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histone H1 - sea urchin (Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accesion: A2550
R;Knowles, J.A.; Childs, G.J.
Nucleic Acids Res. 14, 8121-8133, 1986
A;Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus an
                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q8X965; GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane spanning protein TolA [imported] - Escherichia coli (strain 0157:H7, substrain C;Species Escherichia coli C;Species Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: G85576 C;Accession: G85576 C;Accession: G85576 C; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
                                                                                                                     Ω.
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spanning protein TolA [imported] - Escherichia coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-394 <2TO>
A;Residues: 1-394 <2TO>
A;Cross-references: UNIPROT:Q8X965; GB:AE005174; NID:g12513672; PIDN:AAG55075.1; GSPDB:(A;Experimental source: strain O157:H7, substrain EDL933
A;Genetics:
A;Genetics:
                         C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F90725
BNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and (A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and (A;Accession: F90725
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Reference pubper: Applications ary
A;Reference DNA
A;Residues: 1-394 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKAE----KAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAK-EAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKKEAY-KAEAKKYAKAAKAEKKEYAABEAKK---AEAAKAYKAEAAKAAAKEAA 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.0%; Score 181.5; DB 2; Length 394; 52.2%; Pred. No. 5.3e-05; Live 12; Mismatches 32; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.0%; Score 181.5; DB 2; Length 3 52.2%; Pred. No. 5.3e-05; ive 12; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 52.24
Matches 60; Conservative
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: G85576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60;
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A;Cross-references: UNIPROT:P50600; GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360
A;Experimental source: strain PAO1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gispecies: Salmonella enterica subsp. enterica servora Typhi
A,Note: this species has also been called Salmonella typhi
C,Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C,Accession: AGG592
R,Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davis, P.; Davis, P.; Davis, P.; Davis, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica servor A,Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, I. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A;Reference number: A82950; MuID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tolA protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)
A;Accession: A25550
A;Molecule type: DNA
A;Residues: 1-210 <KNO>
A;Cross-references: UNIPROT:P06144; GB:X04488; NID:g9616; PIDN:CAA28177.1; PID:g9617
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TolA protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E83525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 KKAEKAYAKKAKAAKEK-----KAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 KTEAQKA-RAAAKKAKLAAKKKEQKEKKAAKTKARKEKLAAKKAAKKAAKKVKKPAAKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 KEAYKAEAKKYAKAAKAEKKEYAAAEAKKA-----EAAKAYKAEAAKAAAKEAA 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 347;
                                                                                                                                                                                                                                                                                  Length 210;
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34.5%; Score 179; DB 2; Length 34
Best Local Similarity 49.1%; Pred. No. 6.9e-05;
Matches 54; Conservative 17; Mismatches 29; Indels
                                                                                                                                                                                                                                                                          Score 181; DB 2;
Pred. No. 3.6e-05;
8; Mismatches 36
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Sperm tail-specific protein mst101(2) - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Species: Drosophila hydei
C;Species: Drosophila hydei
C;Date: 19-Uul-1996 #sequence_revision 26-Uul-1996 #text_change 09-Jul-2004
C;Accession: S231364; S34154
R;Neesen, J.; Padmanabhan, S.; Buenemann, H.

Burt. J. Biochem. 225, 1089-1095, 1994
A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represer lipha-helical rods within the extremely elongated spermatozoa of Drosophila hydei.
A;Reference number: S51364; MUID:95045538; PMID:7957199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKAEK----AYAKKAKAAKEKKAYAKKEAKAYKAAE-----AKKKAKAEAKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KYAKKAE-KAYAKKAK--AAKEKKAYAKKEAKAYKAAEAK-KKAKAEAKKYAKEAAK---
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                            50 AKEAAKAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKK-AEAAKAYKAEAAKAAAKEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 --AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - sea urchin (Strongylocentrotus purpuratus)
                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-163,'E',164-236,'Q',237-254,257-320,'E',321-1390 <NEW>
A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
  Length 344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
33.2%; Score 172.5; DB 2;
Best Local Similarity 48.7%; Pred. No. 0.00012;
Matches 55; Conservative 9; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37;
     DB 2;
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33.8%; Score 175.5; DB 2
49.2%; Pred. No. 0.00011;
iive 8; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S51364
A;Status: nucleic acid sequence not shown
A;Molecule type: DN
A;Residues: 1-1390 «NEE>
A;Cross-references: UNIPROT: Q08696; EMBL: X73481
R;Neesen, J; Heinlein, U.A.O.; Buenemann, H.
submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: FlyBase: FBgn0011816
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                histone H1-beta, embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: S34153
A;Accession: S34154
A;Molecule type: DNA
                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: mst101(2)
                                                      58;
     Query Match
                                Local
                              Best Loc
Matches
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S51364
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
R;Pacrebini A. O. Simens Sequence 0. N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, R., Dougan, G.; Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0138
A;Actus: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <KCRN>
A;Crosse-references: UNIPROT:Q8ZGZ2; GB:AL590842; PIDN:CAC89966.1; PID:g15979190; GSPDB:CCGGenetics:
A;Gene: tolA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TolA colicin import membrane protein [imported] - Yersinia pestis (strain C092)
A;Cross-references: GB:AL513382; PIDN:CAD05209.1; PID:g16501979; GSPDB:GN00176
C;Genetics:
A;Gene: STY0793
                                                                                                                                                                                                                                          140 KOAAEQQKIAAAAVAKAKEEQKQAETAAAQAKAEADKIVKAQAEAQKKAEAEAKKEAAVA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 AKAKKEAYKAEAKKYAKAAK-----AEKKEYAAAEAKKAEAAK--AYKAEAAKAAAKEA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 AAAKKQA-DADAKKAVEVAEKAAADAAEKKAAADAE-KKAAAAAKKVAAAAAEAKKKAAAAEA 257
                                                                                                                                                                                                                  9
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C;Species: Drosophila hydei
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession, S34153
Submitted to the EMBL Data Library, June 1993
A;Reference number: S34153
A;Accession: S34153
A;Status: preliminary
                                                                                                                                                                                                               1 AKKYAKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KKYAKKAEKAYAKKAKAKAKEKK-----AYAKKEA-KAYKA-AEAKKKAKAEAKKYAKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                              10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: UNIPROT: Q08695; EMBL: X73480; NID: 9313199; PID: 9313200
                                                                                                                                                                                                                                                                                                                 61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAA---KEAAYE 108
                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                    34.3%; Score 178; DB 2; Length 376;
52.3%; Pred. No. 8.5e-05;
tive 10; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.3%; Score 178; DB 2; Length 388;
52.1%; Pred. No. 8.7e-05;
ive 12; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mst101-1 protein - fruit fly (Drosophila hydei)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: FlyBase:Dhyd/mst101
A;Cross-references: FlyBase:FBgn0011816
C;Superfamily: neurofilament triplet H protein
                                                                                                                                                      58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 52.19
Matches 63; Conservative
                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-344 <NEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 A 106
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                                                                                                                                                        Matches
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histone H1 - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accesion: S55889; S62122
R;Fabry, S.; Mueller, K.; Lindauer, A.; Park, P.B.; Cornelius, T.; Schmitt, R.
Curr. Genet. 28, 333-345, 1995
A;Telte: The organization structure and regulatory elements of Chlamydomonas histone gene A;Reference number: S59581; MUID:96120862; PMID:8590479
A;Retens: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-231 <FAB>
A; Cross-references: UNIPROT: Q39576; EMBL: U16726
A; Note: the authors did not translate the codon for residue 1
R; Fabry, S.; Ford, C.; Lindauer, A.; Mueller, K.; Cornelius, T.; Schmitt, R.
submitted to the EMBL Data Library, October 1994
A; Description: The organization, structure and controlling elements of Chlamydomonas hist
A; Reference number: S62122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Residues: 1-220 <COL>
A,Residues: 1-220 <COL>
A,Cross-references: GB:M17018; NID:g211834; PIDN:AAA48788.1; PID:g211835
C,Superfamily: histone H1
C,Superfamily: histone H1
C,Keywords: accetylated amino end; chromosomal protein; DNA binding; nucleosome; nucleus F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
                                                                                                    1205 AKKAEEE-RKKAEAVK-KAEEAKKKAEAAKKAEERKK-KAEAAKKALERKKKSEAAKKAL 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEA----KAYKAAEAK---KKAKAEAKKYAKEA 53
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A;Cross-references: EMBL:U16726; NID:g571479; PIDN:AAA98452.1; PID:g571480
                                                   5 AKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKKEAYKA-
5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 АКАККЕАУКАЕАККУАКААКАЕККЕУАА-АЕАККАЕААКАУКАЕААКАААКЕ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Indels
31; Indels
                                                                                                                                                                                        64 EAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
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C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 31.8%; Score 165; DB 2;
1 Similarity 46.4%; Pred. No. 0.00038;
52; Conservative 11; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 164.5; DB 2
Pred. No. 0.00042;
54; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.7%;
45.9%;
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Matches 52; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Matches
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HISTORIA PAURIAN

HISTORIA PAURIAN

C.Species: Parechinus angulosus (angulate urchin)

C.Species: Parechinus angulosus (angulate urchin)

C.Species: Jar Mar-1980 #sequence revision 31-Mar-1980 #text_change 09-Jul-2004

C.Accession: A91090; A91091; A0288

R.Strickland, W.N.; Strickland, M.; de Groot, P.C.; von Holt, C.; Wittmann-Liebold, B. Bur J. Blochem. 104, S59-556, 1980

A.Title: The primary structure of histone HI from sperm of the sea urchin Parechinus anguminal cyanogen bromide peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Mesidues: 1-248 < cSTP.
A; Residues: 1-248 < cSTP.
A; Cross-references: UNIPROT: P02256
B; Strickland, W.N.; Strickland, M.; Brandt, W.F.; von Holt, C.; Lehmann, A.; Wittmann-Li
Biochem. 104, 567-578, 1980
A; Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus and A; Reference number: A91091; MUID: 80156832; PMID: 7363905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 KKAKKTSAAAKAKKAKAAAAKKARKAKAAKRKAALAKKKAAAAKRKAAAKAKKKAKEKK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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A;Experimental source: subspecies yoelii; strain YM
                             -AKKKAKAEAKKY 49
                                                                                                                                                               50 AKEAAKAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 62/1; 1648/1; 1674/2; 1697/1
C;Keywords: alternative splicing; cell binding; erythrocyte invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 170.5; DB 2; Length 1701; Pred. No. 0.00076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                           1 AKKYAKKAEKAY----AKKAKAAKEKKAYAKKEAKAYKAAE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Reference number: A91090, MUID:80156831, PMID:67609 A; Contents: sequence of residues 1-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.9%; Score 170.5; DB 1; llarity 46.0%; Pred. No. 0.00018; Conservative 9; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1701 <KAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 80-248 <ST2>
A;Note: 144-Arg was also found
C;Superfamily: histone HI
C;Keywords: DNA binding; nucleosome; sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
Les 52; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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A, Molecule type: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A91091
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Best Local S
Matches 52
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GGCT-4 protein - Chlamydomonas reinhardtii (fragment)
CGGT-8: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S19113; S14466
B;Wakarchuk, W.W.; Mueller, F.W.; Beck, C.F.
B;Makarchuk, W.W.; Mueller, F.W.; Beck, C.F.
A;Makarchuk, W.W.; Mueller, F.W.; Beck, C.F.
A;Accession: S19113
A;Cosserreiminary
A;Wolecule type: DNA
A;Residues: 1-265 <WAK>
A;Residues: 1-265 <WAK>
A;Residues: 1-265 <WAK>
A;Residues: 1-265 <WAK>
A;Groserreiminary
A;Wolecule type: DNA
A;Residues: 1-265 <WAK>
A;Residu
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                                                                                   2 KKYAKKA---EKAYAKKAKAKEKKAYAKKEA----KAYKAAEAKKKAKAEAKKYAKEAA 54
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Best Local Similarity 39.4%; Pred. No. 0.0005;
Matches 50; Conservative 21; Mismatches 38; Indels 18; Gaps
    17; Gaps
    39; Indels
    10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: December 14, 2004, 05:52:15 Job time : 25.0654 secs
56; Conservative
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199 EAKAKEA 205
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220 SA 221
Matches
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Plasmodium yoelii yoelii.
Eukaryotain Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
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01-MAR-2004 (TrEMBLrel. 26, Le
01-MAR-2004 (TrEMBLrel. 26, Le
Erythrocyte binding protein.
Name=PY05977;
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Q7155qB plasmodium
Aq73467 plasmodium
Aq73466 plasmodium
Aq73466 plasmodium
P19934 escherichia
Q8fftt escherichia
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Aas61283 yersinia
Q8zqt salmonla
Q7aq18 escherichia
Q7aq18 escherichia
Q8x565 escherichia
P50600 pseudomonas
Q6d7f3 erwinia car
Q8z8C1 salmonella
Q8z22 yersinia pe
Q8cz8 yersinia pe
Q8cz8 yersinia pe
Q73d27 bacillus ce
Aas3918 bacillus
Q6cdx0 yarrowia 1;
Q6cdx0 yarrowia 1;
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Aar37978 unculture
Q6cgn4 yarrowia li
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07rc08 plasmodium
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                                                                                                                                                ; Search time 122.338 Seconds (without alignments) 512.646 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                          1 AKKYAKKAEKAYAKKAKAK..........AKAYKAEAAKAAAKEAAYEA 109
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Q7c2q4
Q83sa1
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Q7K5Q8
AAQ73467
Q7K5Q7
AAQ73466
Q875G7
Q875T1
Q875T2
Q874W64
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Maximum Match 100%
Listing first 45 summaries
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Q7RC08
Q9WWX1
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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                   09cm70 pasteurella

06hbe7 bacillus th

008696 drosophila

06f986 acinetobact

P02256 parechinus

07kpz1 plasmodium

Aq73456 plasmodium

Aq73455 plasmodium

Aq73457 plasmodiu

061164 plasmodium

061164 plasmodium

061164 plasmodium

061164 plasmodium

061164 plasmodium

0619576 chlamydomon

P15869 strongyloce
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drosophila
pasteurella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pectobacterium.
NCBI_TaxID=556;
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Ray M.C., Vianney A., Cotte-pattat N., Lazzaroni J.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ297885; CAC82708.1; --
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InterPro; IRR010528; TolA.
Pfam; PF06519; TolA; 1.
SEQUENCE 395 AA; 41601 MW; 3COCIDC12E181013 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395 AA
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                                                 QGHHET
MST2_DROHY
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
Tola protein.
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les 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAAAKEAAYEA 109
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Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
Peterson J.D., Pop M., Kosack D.S., Shuwaya M.F., Bidwell S.L.,
Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
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Cumningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
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"Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
Nature 419:12-519(2002)
C.-!- CAUTION: The sequence shown here is derived from an
EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1298 AEEEKKKAEA---AKKAEEEKKKAEAAKKAEBEKKKAEAAKKAEEEKKKAEAAKKAEEE 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 AKKEAYKAEAKKYAKAAKAEKKEYAAA-----EAKKAEAAK----AYKAEAAKAAAKE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKYAKKAEKAYAKKAKAKAKEKKAY-AKKEAKAYKAAEAKKKAKA----EAKKYAKEAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 37.3%; Score 193.5; DB 2; Length 1701;
Best Local Similarity 50.4%; Pred. No. 8.1e-05;
Matches 60; Conservative 12; Mismatches 28; Indels 19; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=mt-2;
MEDLINE=96422022; PubMed=8824639;
Rodriguez-Herva J.J., Ramos J.;
Rodriguez-terva J.D., Ram OprL mull mutant of Pseudomonas putida.";
J. Bacteriol. 178:5836-5840(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AABLO101968; EAA18109.1; -. GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0004872; F:receptor activity; IEA.
GO, GO:0009405; P:pathogenesis; IEA.
Interpro; IFR008602; Duffy_binding.
Pfam; PF05424; Duffy_binding; 1.
SEQUENCE 1701 AA; 197910 MW; 03BE665BAE45C669 CRC64;
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J. Bacteriol. 178:1699-1706(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2004 (TrEMBLrel. 26, Tola protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.
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                                                      PubMed=12368865;
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REPRESENTATIONS OF STATE OF ST
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:000786; C:nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; P:Protein transporte activity; IEA.
GO; GO:000563; P:protein transport; IEA.
GO; GO:0015031; P:protein transport; IEA.
InterPro; IPR016528; TolA.
InterPro; IPR016528; TolA.
InterPro; IPR016528; TolA.
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GO; GO:0000786; C:nucleosome; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0030288; C:poriplaemic space (sensu Gram-negative Bact. . .; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Nelson K.B., Weinel C., Paulsen IT., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
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Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
Fraser C.M.,
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                                                                                                                                                                   Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; X74218; CABS0780.1; -.
HSSP; F50600; 1LRO.
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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TIGREAMS; TIGR01352; tonB_Cterm; 1.
SROUENCE 372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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50.4%; Pred. No. 3.5e-05;
iive 14; Mismatches 31
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Name=tolA; OrderedLocusNames=PP1221;
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Best Local Similarity
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Plasmodium vivax.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5855;
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BMB1, AVG12083; AAQ73467.1; -. InterPrc, FQ42083; AAQ73467.1; -. InterPrc, FQ42083; AAQ73467.1; -. Exequence 1817 AA; 206998 MW; CE2C737CD537E553 CRC64;
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NCBI_TaxID=5855;
                                                                                                                                                                                                                                     372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
    GO, GO:0008365; F:protein transporter activity; IEA. GO; GO:0006334; P:nucleosome assembly; IEA. GO; GO:0015031; P:protein transport; IEA. InterPro; IPR005819; Histone_H5. InterPro; IPR010528; TolA. InterPro; IPR010528; TolA.
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(TrEMBLrel. 27, Last sequence update)
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PRINTS; PR00624; HISTONEHS.
TIGRFAMS; TIGR01352; tonB_Cterm; 1.
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02-MAR-2004 (TrEMBLrel. 27, La
Erythrocyte binding protein 3.
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SEQUENCE 372 AA;
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                                             Michon P., Stevens J.R., Kaneko O., Adams J.H.;
"Evolutionary relationships of conserved cysteine-rich motifs in adhesive molecules of malaria parasites.";
Mol. Biol. 19:112.12.142(2002).
EMBL; AY042083; AAQ73467.1; -. SEQUENCE 1817 AA; 206998 MW; CE2C737CD537E553 CRC64;
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Brolutionary relationships of conserved cysteine-rich motifs in
adhesive molecules of malaria parasites.";
Mol. Biol. Bvol. 19:1128-1142(2002).
EMBL, AY042083, AAQ73466.1; -.
Interpro; IPR011046; WD. 099B2D035391E399 CRC64;
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NCBI_TaxID=5855;
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05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Erythrocyte binding protein 2.
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49.6%; Pred. No. 0.00013;
tive 17; Mismatches 22
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STRAIN=Salvador;
MEDLINE=22077637; PubMed=12082132;
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1320 EDARKA-EEARKAEAAKKAEAARKAEAAKKAEAARKAEAAKKAEEAKKAEAAKKA-EAA 1376
                         51 KEAAKAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAK----AYKAEAAKAAAKEAA 106
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MREDLINES=97061202; PubMed=8905232;
STRAIN=F1051202; PubMed=8905232;
STRAIN=97061202; PubMed=8905232;
STRAIN=97061202; STRAIN BABDA T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itch T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
Yano M., Horiuchi T.;
Yano M., Horiuchi T.;
Sampei G., Seki Y., Pagami H., Takemoto K., Wada C., Yamamoto Y.,
Nano M., Horiuchi T.;
Sano M.,
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Levengood S.K., Webster R.E., "Nucleotide sequences of the tolA and tolB genes and localization their products, components of a multistep translocation system in Escherichia coli.";
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Enterobacteriaceae, Escherichia.
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Name=tola; Synonyms=cim, excC, lky; OrderedLocusNames=b0739;
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                                                                                                                                                                                                                                                                            421 AA.
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STRAIN=K12 / JM105;
MEDLINE=90078104; Pubmed=2687247;
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MRDLINE=97133271; PubMed=8978668;
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MEDLINE=22077637; PubMed=12082132;

MEDLINE=22077637; PubMed=12082132;

Michon P., Stevens J.R., Kaneko O., Adams J.H.;

T adhesive molecules of malaria parasites.";

Mol. Biol. Evol. 19:1128-1142(2002).

R Mol. Biol. Evol. 19:1128-1142(2002).

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

R GO; GO:0004872; P:receptor activity; IEA.

R GO; GO:0016021; Diathogenesis; IEA.

R Diathogenesis; IEA.
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"Evolutionary relationships of conserved cysteine-rich motifs in adhesive molecules of malaria parasites.";
MOI. Biol. Evol. 19:1128-1142(2002).
EMBL; AX042083; AAQ73466.1; -.
SEQUENCE 1830 AA; 208690 MW; 099B2D035391E399 CRC64;
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5855;
                                                                                                                                                                                                          Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-07N-2002 (TrEMBLrel. 21, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Erythrocyte binding protein 1.
                                                                                        02-MAR-2004 (TrEMBLrel. 27, Last sequence update) 02-MAR-2004 (TrEMBLrel. 27, Last annotation update) Erythrocyte binding protein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.7%; Score 190.5; DB 2
49.6%; Pred. No. 0.00013;
tive 17; Mismatches 22
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                           1830 AA
                                                                     Created)
                                                                                                                                                                                                                                                                                              STRAIN=Salvador;
MEDLINE=22077637; Pubmed=12082132;
                                                                   (TrEMBLrel. 27,
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                                                                                                                                                                                   Plasmodium vivax.
                                                                                                                                                                                                                        NCBI_TaxID=5855;
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                                                                 02-MAR-2004
02-MAR-2004
02-MAR-2004
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                                                AAQ73466;
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                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
"Filamentous phage infection: crystal structure of g3p in complex with its coreceptor, the C-terminal domain of TolA."; Structure 7:711-722(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Periplasmic (Potential).
DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
13 tandem repeats of [EDA]-K(1,2)-A(2,4).
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Ecodene; EG11007; tola.

InterPro; IPR010528; TolA.

Pfam; PF06519; TolA; 1.

3D-structure; Bacteriocin transport; Complete proteome;

Inner membrane; Protein transport; Repeat; Transmembrane; Transport.

Cytoplasmic (Potential).

1 13 Cytoplasmic (Potential).

24 Potential.
                                                            FUNCTION: Involved in the tonB-independent uptake of group A colicins (colicins A, E1, E2, E3, and K). Necessary for the colicins to reach their respective targets after initial binding to the bacteria. Also involved in the translocation of
                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                                                    bacteriophage DNA.
SUBUNIT: Interacts, via domain II, with porins ompC, phoE and
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EMBL, BAR00177; AAC73833.1; -.
EMBL, D90713; BAA35405.1; -.
PIR, JV0057; JV0057.
PDB; ITOL, X-ray; A=-.
ECHOBASE; EB1000; -.
ECHOBASE; EB1000; -.
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Best Local Similarity
Matches 61; Conserv
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=06.H1 / CFT073 / ATCC 700928;

MACH R.A., Burland V., Plunkett S.

MACH R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

MAYNEW G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

MODISY H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

REMBL; ARD165757; AAN79291.1; -.

RESP, P19934; ITOL.

InterPro, IPR010528; TolA.

Refam; PR06519; TolA.

Refam; PR06519; TolA; 1.

SEQUENCE 421 AA, 43184 MW, DB296626F056D385 CRC64;
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SONG Y., TONG Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
Han Y., Pang X., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
Yang R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017130; AAS61283.1;
InterPro; IPR010528; TolA.
Pfem; PF06519; TolA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 AAAEAQKKAEAAAALKKKAEAABAAABAKKKAATEAAEKAKAEAEKKAAAEKA 232
                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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Enterobacteriaceae; Yersinia.
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
TolA colicin import membrane protein.
Name=tolA, OrderedLocusNames=YP1033;
                                                                                                                                                                             (TrEMBLrel. 23, Last sequence update) (TrEMBLrel. 26, Last annotation update)
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53.0%; Pred. No. 5.2e-05;
iive 11; Mismatches 32;
                                                                                                              421 AA
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                                                                                                                                                                                                                                           Name=tolA; OrderedLocusNames=c0818;
Escherichia coli 06.
                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=217992;
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MBDLINE=21534948; PubMed=11677609;
MBDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last aenotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tol protein, membrane spanning protein.
Name=tolA; OrderedLocusNames=STM0747;
Salmonellat typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
NCBI_TaxID=632;
                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Indels 11;
                                                                                        35.9%; Score 186.5; DB 2; Length 401; 52.6%; Pred. No. 6.8e-05; ative 12; Mismatches 31; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 35.9%; Score 186.5; DB 2; Length 401; Local Similarity 52.6%; Pred. No. 6.8e-05; les 60; Conservative 12; Mismatches 31; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang R.; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
41868 MW; 43D682DE91CF1301 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE017130; AAS61283.1; -.
SEQUENCE 401 AA; 41868 MW; 43D682DE91CF1301 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-WAR-2004 (TrEMBLrel. 27, Created)
24-WAR-2004 (TrEMBLrel. 27, Last sequence update)
04-WAY-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                     60; Conservative
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401 AA;
                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS61283;
SEQUENCE
                                                                                        Query Match
Best Local S
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                                                                                                                                                                                     Matches
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082076
002076
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DT 01
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AAS61283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYK-AAEAKKKAKAEAKKYAKEA-AKAKK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 EAYK--AEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAK---AAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 EAAKAAABAKKKAEBABAAK----AAAEAKKKADAEAAKA-AAEAKKKKADAAAAKAAAEA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=015:471, RIND 0509952 / EHEC;
MEDLINE=2115:621; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterchemorrhagic Escherichia coli "Complete genome sequence of enterchemorrhagic Escherichia Coli "Colification with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.,, Wilson R.K.; Remonella enterica serovar Typhimurium "Complete genome sequence of Salmonella enterica serovar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                ch 35.5%; Score 184.5; DB 2; Length 407; I Similarity 55.5%; Pred. No. 9.3e-05; 66; Conservative 11; Mismatches 25; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.0%; Score 181.5; DB 2; Length 394; 52.2%; Pred. No. 0.00014; Live 12; Mismatches 32; Indels 11.
                                                                                                                                                                                                                                                                                                                      407 AA; 41865 MW; 2534352116602D75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40517 MW; 5B58D8E8230BDE28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Membrane spanning protein Tola.
OrderedLocusNames=EC80774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AP002553; BAB34197.1; -.
InterPro; IPRO10528; TolA.
Pfan, PF06519; TolA; 1.
SEQUENCE 394 AA, 40517 MW;
                                                                                                           Nature 413:852-856(2001).
EMBL; AE008730; AAL19691.1;
HSSP; P19934; 1TOL.
                                                                                                                                                                                                        InterPro; IPR010528; TolA. Pfam; PF06519; TolA; Complete proteome. SEQUENCE 407 AA; 41865
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Matches 60; Conserva
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5.1.6
Compugen Ltd.
version :
- 2004 (
GenCore (c) 1993
        Copyright
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OM protein - protein search, using sw model

December 14, 2004, 05:47:53 ; Search time 120.498 Seconds (without alignments) 324.499 Million cell updates/sec Run on:

US-10-792-311-7 519 Title: Perfect score:

1 AKKYAKKAEKAYAKKAKAAK......AKAYKAEAAKAAAKEAAYEA 109 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A Geneseq 23Sep04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

	Description	Aay82577 Copolymer		-	Aay82574 Copolymer	Aar06445 Recombina	Abo67048 Klebsiell	Abu40185 Protein e	Abu27824 Protein e	Abu28559 Protein e	Aar06446 Recombina	Abu47123 Protein e	7	Aay82573 Copolymer	σ	4		σ	m	Abj18771 Pseudomon	Abo80835 Pseudomon	Aay14928 Amino aci	Abp70903 Mycobacte	Abu47848 Protein e	Abu50266 Protein e	Abu44721 Protein e
SUMMAKIES	ID	AAY82577	AAY82576	AAY82575	AAY82574	AAR06445	ABO67048	ABU40185	ABU27824	ABU28559	AAR06446	ABU47123	ABU31397	AAY82573	AAY98499	AAY59044	AAB45852	AAU04289	ABU38313	ABJ18771	ABO80835	AAY14928	ABP70903	ABU47848	ABU50266	ABU44721
	DB	٣	m	m	ო	~	7	9	9	9	7	9	9	m	m	٣	4	4	9	9	7	~	φ	φ	9	φ
	Query Match Length DB	109	98	77	99	154	469	372	428	421	106	407	323	26	100	100	100	100	347	347	407	223	223	376	388	387
de	Query Match	100.0	60.2	55.7	44.0	40.3	37.8	36.7	36.6	36.5	36.0	35.5	35.0	34.8	34.6	34.6	34.6	34.6	34.5	34.5	34.5	34.3	34.3	34.3	34.3	33.5
	Score	519	312.5	289	228.5	209	196	190.5	190	189.5	187	184.5	181.5	180.5	179.5	179.5	179.5	179.5	179	179	179	178	178	178	178	174
	Result No.	-1	7	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abu39221 Protein e Adf05105 Bacterial		Abu42038 Protein e	Aar84568 Trypanoso	Abu49418 Protein e	Abo23526 Vibrio ch	Abm67869 Photorhab	Aay34068 Histone H	Aay57366 Human his	Aay34060 Human his	Aay57358 Human his	Adq09196 Human H1F	Ada35034 Acinetoba	Ada33882 Acinetoba	Aae13234 Human lin	Aau09944 Histone H	Add22892 Human his	Aar84569 Trypanoso	Aaw29477 Human his
ABU39221 ADF05105	ABU17340	ABU42038	AAR84568	ABU49418	AB023526	ABM67869	AAY34068	AAY57366	AAY34060	AAY57358	ADQ09196	ADA35034	ADA33882	AAE13234	AAU09944	ADD22892	AAR84569	AAW29477
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389	448	336	643	356	356	357	158	158	226	226	226	468	214	234	234	234	472	218
33.4	31.5	31.4	31.3	31.2	31.2	31.0	30.9	30.9	30.9	30.9	30.9	30.9	30.8	30.7	30.7	30.7	30.5	30.4
173.5	163.5	163	162.5	162	162	161	160.5	160.5	160.5	160.5	160.5	160.5	160	159.5	159.5	159.5	158.5	158
26	8 9	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7. AAY82577 standard; peptide; 109 AA 28-JUL-2000 (first entry) AAY82577; AAY82577

Unidentified.

WO200018794-A1.

06-APR-2000.

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; Gad A,

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

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treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include aither cell—mediated or antibody—mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, conteact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic mysachema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythemacosus. Mediated mediated diseases which can be treated include host-versus-graft disease, polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
   the invention are used as molecular weight markers for glatiramer
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Sequence 109 AA;

9 1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60 1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA Gaps . 0 61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109 Length 109; 0; Indels 100.0%; Score 519; DB 3; 100.0%; Pred. No. 3.9e-36; iive 0; Mismatches 0; Query Match Best Local Similarity 100.0 Matches 109, Conservative g 8 셤 à

RESULT

AAY82576 standard; peptide; 86 AA

AAY82576;

(first entry) 28-JUL-2000 Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.

Copolymer; molecular weight marker; TV-marker; immune dieease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; soteopathic; immunosuppressive; antithyrocid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidabetic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; didopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. AAY 82577
XXX AAY 82577
AAY 82577
AAY 82577
AAY 82577
AAY 82577
AAY 8277
AA

Unidentified

NO200018794-A1

06-APR-2000

99WO-US022402. 24-SEP-1999;

98US-0101693P. 25-SEP-1998;

(YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; Gad A, WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

```
weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amone acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer cateatate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include aither cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thrombocytopaenia purpura, collitis, contact sensitivity disease, dispathic mycoedema, myasthenia gravis, syndrome, Hashimoto's disease, idiopathic mycoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated disease, and delayed-type hypersensitivity. The copypeptides of the invention have defined molecular weights and physical
                                                                               AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
                          Claim 10; Page 14; 72pp; English.
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Sequence 86 AA;

5 36 1 AKKYAKKAEKAYAKKAKAYEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKA 60 1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKA---------27; Gaps 61 YKAEAKKYAKAAKAEKKEYAAAEAK-KAEAA-KAYKAEAAKAAAKEAAYEA 109 60.2%; Score 312.5; DB 3; Length 86; 72.1%; Pred. No. 5e-19; Indels 3, 1; Mismatches 80; Conservative Query Match Best Local Similarity Matches 80; Conserv 셤 ð g ò

AAY82575

AAY82575 standard; peptide; 77 AA.

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.

glatizamer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatorid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Gulllain-Barre's syndrome; psoriasis; Copolymer; molecular weight marker; TV-marker; immune disease; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified

WO200018794-A1

06-APR-2000.

99WO-US022402 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD.

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer of the invention are used as molecular weight markers for glatizamer created terrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arbritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, peoriasis, pemphigus vulgaris, or systemic lupus erythemacosus. Mediated mediated disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical
                                                                                                                                                    Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                   Claim 10; Page 14; 72pp; English.
(TEVA-) TEVA PHARM USA INC
                                                                                                   WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 77 AA;
                                                   Lis D;
                                                   3ad A,
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---- 36 1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 3; Indels 32; 61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109 Score 289; DB 3; Length 77; Pred. No. 4.1e-17; 1; Mismatches 3; Indels 55.7%; Local Similarity 67.0 es 73; Conservative Query Match **datches** a 8 셤

4; 9

> AAY82574 standard; peptide; 66 AAY82574; RESULT 4 AAY82574
> XXX
> XXX
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> 28.
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28-JUL-2000 (first entry)

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; auttoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4. pemphigus vulgaris; systemic lupus erythematosus

Unidentified

Synthetic

WO200018794-A1

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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight TV-marker polypeptides (1) for determining the molecular weight invention describes polypeptides (1) for determining the molecular weight and an amone acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer of the invention are used as molecular weight markers for glatizamer to treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases include arthritic conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thrombocytopaenia purpura, colitis, Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, diabetes mellitus, Graves disease, pardrome, Habhimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated disease, which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The collyperties of the invention have defined molecular weights and physical makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
                                                                                                                                                                                                                                                                                                                                                                                                          AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.0%; Score 228.5; DB 3; Length 66; 56.9%; Pred. No. 3.8e-12; ive 0; Mismatches 4; Indels 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant copolymer 1-77, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKK-EKAYAKAKKA-----EAKAAKKA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR06445 standard; protein; 154 AA
                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 14; 72pp; English.
                                                                                                                                               (YEDA ) YEDA RES & DEV CO LTD.
(TEVA-) TEVA PHARM USA INC.
                                                            99WO-US022402.
                                                                                                       98US-0101693P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                      WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 66 AA;
                                                                                                                                                                                                                Lis D;
                                                            24-SEP-1999;
                                                                                                       25-SEP-1998;
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                 06-APR-2000.
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                                                                                                                                                                                                                Gad A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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(ELIT-) ELITRA PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                        for improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 Usg491009, NRKL B-15910), a plasmid used to express Protein A.

The resulting plasmids encode fusion proteins consisting of beta-current between the Protein A, and rCOP-1 sequences. A methionine residue cocurs between the Protein A and rCOP-1 sequences, originating from the current between the Protein A and rCOP-1 sequences, originating from the cocurs between the Protein A and rCOP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-77 contains oligonucleotide duplakes incoding the following segments: YKK, EAE, KAK, AAK, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the fusion protein. The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain amino acids. See also AAQ05665. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 EYKKKAKAAABABEABYKKEABEABYKKYKKKAKKAKKAKYKKKAKEABEKAKAAABEABKAKBABEYK 141
                                                                                                                                                                                                             Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKYAKKAEKA-----YAKKAKAKAKEKKAYA----KKEAKAYKAAEA-----KKKAK-A 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 KKKAKEAEKAKKAKYKKYKKEAEAAKAAAAAAAAYKKEAEA--AAEAEKAKYKKKAKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAKKYAKEAAKA - - KKEAYKAEAKKYAKAAKAEK - - - - - - - KEYAAAEAKKAEAA - - K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 209; DB 2; Length 154; Pred. No. 3.9e-10; 8; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klebsiella pneumoniae polypeptide seqid 13565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABO67048 standard; protein; 469 AA.
                                                                                                                                                                                                                                                  Disclosure; Fig 11; 25pp; English.
                                                    90EP-00301700
                                                                                         90US-00473845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 53.7%;
Matches 72; Conservative
                                                                            89US-00312541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 AYKAEAAKAAAKEA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 KYKKEAEK--AKEA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klebsiella pneumoniae
                                                                                                                 (REPK ) REPLIGEN CORP
                                                                                                                                                                    WPI; 1990-255848/34.
                                                                                                                                                                                   N-PSDB; AAQ05664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-2004
                                                  16-FEB-1990;
                                                                                         07-FEB-1990;
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                                                                            17-FEB-1989;
                          22-AUG-1990
EP383620-A.
                                                                                                                                                                                                          Producing
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                                                                                                                                             Cook KS;
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                                                                                                                                                                                                                                                                                                                                                                           useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 AKAKKEAYKAEAKKYAKA---AKAEKKEYAAAEAKKAEAAKAYKA--EAAKAAAKEAAYE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 ADAKKQAEAAAAAKAAAEAKKQAEAEAAKAAAEAQKKAEAAAAKKAQQEAEKKAQOEAAKQ 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKAEKAYAKKAKAKEKEK---KAYAKKEAKAYKAAEAKKKAKAEAK----KYAKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding a Klebsiella pneumoniae polypeptide, preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #25712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.8%; Score 196; DB 7;
51.2%; Pred. No. 1.5e-08;
iive 12; Mismatches 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 13565; 932pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU40185 standard; protein; 372 AA.
                                                                                                                                                                        (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362859P.
                                                                                                               99US-0117747P
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                                                         27-JAN-2000; 2000US-00489039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Matches 62; Conservative
                                                                                                                                                                                                                                 Osborne M;
                                                                                                                                                                                                                                                                                       WPI; 2003-895346/82
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                                                                                                                                                                                                                                                                                                                  N-PSDB; ABD00619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 469 AA;
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                                                                                                               29-JAN-1999;
26-AUG-2003.
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ftp.wipo.int/pub/published_pct_sequences Sequence 372 AA; in electronic ABU27824; Query Match Matches ઠે 셤 ઠ g

the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

cof the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

cnoclaing a polypeptide whose expression is inhibited by the antisense

cnucleic acid; (2) a host cell contaning the vector; (3) an isolated

contisense nucleic acid; (4) an antibody capable of specifically binding

cn the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

cr proliferation or the activity of a gene in an operon required for

proliferation or that has an activity against a biological pathway

cr proliferation; (7) identifying a compound that influences the activity of

the gene product or that has an activity against a biological pathway

cr proliferation or that has an activity against a biological pathway

cr proliferation or that inhibits cellular proliferation; (8)

dentifying a gene required for cellular proliferation of an

cr pathway in which a proliferation-required gene or its gene product lies

cr a gene on which the test compound that inhibits proliferation of an

cr organism acts; (9) manufacturing an antibiotic; (10) profiling a

compound's activity; (11) a culture comprising strains in which the gene

product is overexpressed or underexpressed; (12) determining the extent

cr product is overexpressed or underexpressed; (12) determining the extent

cr proliferation of an organism. The antisense nucleic acids are useful for

dentifying proteins or screening for homologous nucleic acids required

cr for cellular proliferation or homologous nucleic acids required

cr for cellular proliferation or homologous nucleic acids required

cr for cellular proliferation or homologous nucleic acids required

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the invention fraintes to an isolated mucienc acid comprising any one or the invention fraintes to an isolated mucienc acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular completed proliferation or that has an activity against a biological pathway are proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound; a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound; a contrains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational conditions of strains; or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. K. pneumoniae or P. aeruginosa. The present sequence data for this patent in a present a geneen or the present ageneen or product or the present sequence data for this patent of the princed specification, but was obtained tor parent proversy programs, or for screening the se
                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
Zyskind JW;
Xu HH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to an isolated nucleic acid comprising any
     $ $
Ohlsen |
Forsyth |
Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID NO 68109; 1766pp; English
     Malone C,
Carr GJ,
Zamudio C,
Trawick JD,
                                                                                                                                            2003-029926/02
                                                                                                                                                                                         N-PSDB; ACA44055
     μÖ
     Wang
Wall
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screening

New antisense nucleic acids, useful for identifying proteins or e for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD, 2003-029926/02.

Wang L,

N-PSDB; ACA31694

(ELIT-) ELITRA PHARM INC.

21-MAR-2001, 2001US-00815242. 06-SEP-2001, 2001US-0094893. 25-OCT-2001, 2001US-0342921P. 08-FEB-2002, 2002US-0372851. 06-MAR-2002, 2002US-0362699P.

21-MAR-2002; 2002WO-US009107.

WO200277183-A2 03-OCT-2002 The invention relates to an isolated nucleic acid comprising any one of

Claim 25; SEQ ID NO 55748; 1766pp; English.

54 55 K--AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKEAAYEA 109 5 AKKAEKAYAKKAKAAK----EKKAYAKKEAKAYKAAE-----AKKKAKAEAKKYAKEAA 13; Gaps 36.7%; Score 190.5; DB 6; Length 372; 50.4%; Pred. No. 3.4e-08; ive 14; Mismatches 31; Indels 13 59; Conservative Local Similarity

directly from WIPO at

drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium,

Æ ABU27824 standard; protein; 428 Antisense; prokaryotic essential gene; cell proliferation; drug design.

Enterobacter cloacae.

Protein encoded by Prokaryotic essential gene #13351

19-JUN-2003 (first entry)

K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences 48 KYAKEAAKAEKKEAYKAEAKKYAKAAKAEKKEYAAAEA----KKAEAAKA---YKAEAAKA 100 225 KAAAEAAKKAAAAEKAAAAEKAAAAKKAAAAEKAAABKKAAABKKAAABKKAAABKA 167 АККАААDAQKKAEAEAAKKAAADAQKKAEAEAAKKA--АADAQKKAEAEAAKKAAQEAEK 224 1 AKKYA----KKAEKAYAKKAKAKAYAKKEAKAYKAAEAKKKAKAEA-----K 47 Gaps 22; Length 428; 32; Indels 36.6%; Score 190; DB 6; 50.8%; Pred. No. 4.4e-08; iive 8; Mismatches 32 DB 6; 64; Conservative Query Match Best Local Similarity Matches 64; Conserv Sequence 428 AA; ò 셤 ò 셤

patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 421 AA;

Length 421;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #14086.
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Yamamoto R,
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                                                                                                                                                                                                                                                        ABU28559 standard; protein; 421 AA
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
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                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Trawick JD,
101 AAKEAA 106
                                                                    285 AAKKAA 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
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Wall D,
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ABU28559
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To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subcloned from pREV 2.1 to pEG3-2deltaN (deposit: 20-NOV-1984 U54691009, NRRL B-15910), a plasmid used to express Protein A. NOV-1984 U54691009, NRRL B-15910), a plasmid used to express Protein A. OV-1984 U54691009, NRRL B-15910), a plasmid used to express Protein A. OV-1984 U54691009, NRRL B-15910), a plasmid used to express Protein A. and rCOP-1 sequences. A methionine residue cocurs between the Protein A and rCOP-1 sequences, originating from the cocurs between the Protein A and rCOP-1 sequences, originating from the companie the following segments: YKK, AAE, KAK, KKA, YEA, YEA, AKA KEA, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the fusion protein. The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain amino acids. See also AAQ05664. (Updated on 25-MAR-2003 to correct PA
                                           5
                                                                                                                      120 AEEAAKOAELKOKOAEEAAAKAAADAKAKAEADAKA--AEEAAKKAAADAKKKAEAEAAK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis.
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                                           Gaps
                                                                                                                                                                                  56 AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant copolymer 1-19, myelin basic protein analogue.
                                         Indels
Query Match 36.5%; Score 189.5; DB (
Best Local Similarity 53.0%; Pred. No. 4.7e-08;
Matches 61; Conservative 11; Mismatches 32
                                                                                                                                                                                                                                                                                                    AAR06446 standard; protein; 106 AA
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90US-00473845.
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Wang |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the 6113 antisease sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a
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Xu HH;
                                                                                                              Gaps
                                                                                                            18;
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                                                                                                                                                                                                                                                                          Query Match 36.0%; Score 187; DB 2; Length 106; Best Local Similarity 55.0%; Pred. No. 1.8e-08; Matches 60; Conservative 11; Mismatches 20; Indels
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Forsyth RA,
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Yamamoto R,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362851.
06-MAR-2002; 2002US-0362699P.
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Trawick JD,
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                     Sequence 106 AA;
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                                                                                                                                                                                                                                  drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
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Xu HH;
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for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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Forsyth RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.5%; Score 184.5; DB (55.5%; Pred. No. 1.2e-07; ive 11; Mismatches 25
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Yamamoto R,
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klebsiella pneumoniae.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-029926/02.
N-PSDB; ACA35267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 407 AA;
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Best Local S
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conding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated publypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation, (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound; a culture or collection of the strains is present in a culture or collection of category or strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, content effect prokent prokaryotic essential genes. Note: The sequence data for this patent did not forme part of the printed specification, but was obtained for the print of the printed specification, but was obtained for the compound and proved the compound an
vector comprising a promoter operably linked to the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 323 AA;
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47 ADAQAKAAEQAAAKAAADAK-KQAEA---AAAKAAAEAKKQAEAEAAKAAAEAQKKAEAA 102 55 1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK----34; Indels 11; Gaps 56 -AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106 103 AAKKAQQEAEKKAQQEAAKQAAAEKAAAB-KAAEKAAAQKAAAEKAAA 153 Score 181.5; DB 6; Length 323; Pred. No. 1.7e-07; 8; Mismatches 35.0%; Ouery Match Best Local Similarity 52.77 Matches 59, Conservative 셤 ઠે

Sequence 56 AA;

AAY82573 standard; peptide; 56 AA AAY82573; RESULT 13 AAY82573

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.

glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antiporiatic; dermatory; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; didopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer; molecular weight marker; TV-marker; immune disease;

Unidentified

WO200018794-A1

06-APR-2000.

99WO-US022402. 24-SEP-1999;

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer accetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases of treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating completed of diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune thyroidmine haemolytic anaemia, autoimmune thyroidmines, e.g. multiple sclerosis, contact cophoritis, autoimmune thyroidmines, e.g. multiples sclerosis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which are abe treated include host-versus-graft disease, cromorations and delayed-type hypersensitivity. The properties which are analogous to glatiramer accetate molecules, which correct complex properties mediated makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                  Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                                                                                                                                                                         Claim 10; Page 14; 72pp; English.
                                                  (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
  98US-0101693P
                                                                                                                                                                                WPI; 2000-317499/27.
                                                                                                                                   Lis D;
25-SEP-1998;
                                                                                                                                 Gad A,
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1 AKKYAKKAEKAYAKKAKAKAKEYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60 --- 39 53; Gaps 61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109 1 AKKYAKK-EKAYAKKA-----EKAAKKAEAKAYKAAEAKKKAEAK-----------YKAEAAKEAAKEAAYEA 56 Length 56; Indels 34.8%; Score 180.5; DB 3; 45.9%; Pred. No. 3.2e-08; live 3; Mismatches 3; 50; Conservative Query Match Best Local Similarity Matches 9 ઠ

AAY98499 standard; peptide; 100 AA AAY98499; RESULT 14

Peptide #10 used in nucleic acid transporter system. 31-JUL-2000 (first entry)

Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.

Synthetic.

07-MAR-2000

93US-00167641. 14-DEC-1993; Smith LC;

Sparrow J,

Gottchalk S,

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Nucleic acid transport system; NTS; cell surface receptor; cytosis; nuclear membrane; lysis moiety; transgenic animal; human disease; nucleic acid delivery; cancer.
                                                                                                                                                                                                                                                                                                                          Amino acid polymer seq ID NO: 64 of US5994109.
                                                                                                                                                                                                                                                                                        AAY59044 standard; peptide; 100 AA
92US-00855389.
93WO-US002725.
                                                                                                                                                                                                                                                                                                              07-MAR-2000 (first entry)
                                                                                                                                                                                                               55; Conservative
                                       WPI; 2000-281993/24.
                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                         Sequence 100 AA;
                            Sottchalk S,
20-MAR-1992;
     19-MAR-1993;
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The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moviment through a nuclear membrane; and/or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytoplasm of the cell. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting specific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells. The NTS can be used in vitro with tissue culture cells. The yes agent within the NTS avoids the problem of endosomal/lysosomal
                                                                                                                                                                                                                                                                                                                                                  Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Col 123-124; 107pp; English.
                                                                                                                                                                            BAYU ) BAYLOR COLLEGE MEDICINE
95US-00460890.
                                                                                      93WO-US002725.
                                                                                                                 93US-00167641.
                                                          92US-00855389.
                                                                                                                                                                                                                                      Cristiano RJ,
                                                                                                                                                                                                                                                                                                WPI; 2000-038262/03.
   03-JUN-1995;
                                                          20-MAR-1992;
                                                                                      19-MAR-1993;
                                                                                                                    14-DEC-1993;
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                                                                                                                                                                                                                                      WOO SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a sufface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36633-A36652 and peptide sequences AAY98456-Y98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      systems are also used to create transgenic animals (as models for human carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEAYKAE
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Н
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.6%; Score 179.5; DB 3; Length 100; 55.0%; Pred. No. 7.2e-08; ative 8; Mismatches 34; Indels 3
                                                                                                                                                   Smith LC;
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                                                                                                                                                Sparrow J, Cristiano RJ, Woo SLC,
                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Col 125-128; 108pp; English
                                                                                      (BAYU ) BAYLOR COLLEGE MEDICINE
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6 KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAE 64
                                                                                                                                            3; Gaps
                                      DB 3; Length 100;
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                                    34.6%; Score 179.5; DB 3
55.0%; Pred. No. 7.2e-08;
tive 8; Mismatches 34
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Sequence 100 AA;
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Sequence 7, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 68109, A
Sequence 55748, A
Sequence 55748, A
Sequence 59321, A
Sequence 75047, A
Sequence 120, Appli
Sequence 120, Appli
Sequence 6237, A
                                                                                                                                               December 14, 2004, 05:52:22; Search time 270.43 Seconds (without alignments) 143.965 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                         1 AKKYAKKAEKAYAKKAKAAK.......AKAYKAEAAKAAAKEAAYEA 109
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(cgnz 6/ptodata1/pubpaa/US07_NEW_PUB.pep:*
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US-09-816-989A-6
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US-09-816-989A-4
US-09-816-989A-4
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Gapop 10.0 , Gapext 0.5
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			equence 7264	Sequence 67145, A	Sequence 45264, A	69962	9889	27, 7	7734	40	32	38	Sequence 1, Appli	Sequence 2, Appli	Sequence 4, Appli	48		297	20	36,		'n		24,	95,	76	8,	16,	19	64969	Sequence 3, Appli
-10-205-979-52	9 6	-10-282-1	-10-282-1	-10-282-1	-10-	-10 - 282 - 1	-10-	-09-820-	US-10-282-122A-77342	-10-229-	US-10-229-567-32	m	US-10-262-209-1	US-10-240-430-2	US-10-229-567-4	-10-733-878-	-10-425-114-5	구	-10-726-692-5	-10-726-692-3	- 1	-10-2	US-10-437-963-186290		•	US-10-282-122A-76514	9-60	4	US-10-437-963-193381	-10-282-1	US-10-229-567-3
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	178	8/1	174	173.5	163.5	163	163	162	162	160.5	160.5	160.5	159.5	159.5	158	158	156.5	156.5	155.5	155.5	154.5	154.5	154.5	154.5	153.5	153.5	153.5	153.5	153.5	153	152.5
14	15	91	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 7, Application US/0981698A

Facent No. US20020115103A1

GENERAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

TITLE OF INVENTION: 2001-03-23

CURRENT FILING DATE: 1998-09-25

PRIOR PELICATION NUMBER: PCT/US99/22402

PRIOR APPLICATION NUMBER: PCT/US99/22402

PRIOR PLING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Version 3.1

SEQ ID NO: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-4-PCT-USE
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR PILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 4
LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                       -- 36
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, OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                      61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
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                                                                                                                     37 -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAKEAAYEA 77
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                          1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKA
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44.0%; Score 228.5; DB 9;
Best Local Similarity 56.9%; Pred. No. 3.6e-11;
Matches 62; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKK-EKAYAKKA------EAKAAKKA---
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 68109, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FLILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                                                               Sequence 4, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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ORGANISM: Artificial Sequence
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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                                                                                                                                                                                                   RESULT 4
US-09-816-989A-4
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APPLICANT:
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APPLICANT: Gad, Ackander
APPLICANT: Lis, Doris
APPLICANT: Lis, Doris
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: 08/09/816,989A
CURRENT FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PARENTIN Version 3:1
SEQ ID NO 5:
LENGTH: 77
                                                                                                                                                                                                                     APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 05/10,693
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 6
LENGTH: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAAKEAAYEA 86
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61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
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Pred. No. 7.9e-16;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 312.5; DB 9
Pred. No. 1.3e-17;
1; Mismatches 3
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; Patent No. US20020115103A1
                                                                                                                     ; Sequence 6, Application US/09816989A; Patent No. US20020115103A1
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 67.0%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 72.1
Matches 80; Conservative
                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
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                                                                        RESULT 2
US-09-816-989A-6
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TYPE: PRT; ORGANISM: Enterobacter cloacae US-10-282-122A-55748
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeelbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Frawick, Sobert
APPLICANT: Frawick, Sobert
APPLICANT: Forsyth, R.
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Best Local Similarity
Matches 64; Conserva
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APPLICANT:
APPLICANT:
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APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
CURRENT ELLITRA.034A
CURRENT APPLICATION NUMBER: US/10/22,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-09-06
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/233,625
PRIOR PLILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
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PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-09

PRIOR PLILING DATE: 2000-09-09

PRIOR PLILING DATE: 2000-10-23

PRIOR PLILING DATE: 2000-11-27

PRIOR PLILING DATE: 2000-11-27

PRIOR PLILING DATE: 2000-11-27

PRIOR PLILING DATE: 2000-12-22

PRIOR PLILING DATE: 2001-12-27

PRIOR PLILING DATE: 2001-02-09

PRIOR PLILING DATE: 2001-02-09

PRIOR PLILING DATE: 2010-10-20

PRIOR PLILING DATE: 2010-10-20

PRIOR PLILING DATE: 2010-10-20

PRIOR PLING DATE: 2010-10-216

PRIOR PLING DATE: 2010-10-216

PRIOR PLING DATE: 2010-30-16

PRIOR SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 36.7%; Score 190.5; DB 15; Length 372; Best Local Similarity 50.4%; Pred. No. 2e-07; Matches 59; Conservative 14; Mismatches 31; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 55748. Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olisen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-68109
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APPLICANT:
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CURRENT APPLICATION: IGENILITICATION OF ESSENTIAL Genes in Microorganisms
FILE REFERENCE: ELITRA, 0.34A

CURRENT PELING DATE: 2003-02-20

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-10-23

PRIOR PLICATION NUMBER: 60/242,58

PRIOR PLICATION NUMBER: 60/242,58

PRIOR FILING DATE: 2000-11-22

PRIOR PLICATION NUMBER: 60/257,931

PRIOR PLING DATE: 2000-11-2-22

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
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                                                                                                                                                                                                                                               Length 421;
                                                                                                                                                                                                                                                                                                       32; Indels
                                                                                                                                                                                                                                               DB 15;
                                                                                                                                                                                                                                                                     .7e-07;
                                                                                                                                                                                                                                                                                                       11; Mismatches
                                                                                                                                                                                                                                           36.5%; Score 189.5; 53.0%; Pred. No. 2.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 75047, Application US/10282122A; Publication No. US20040029129A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Salmonella typhimurium
                            SOFTWARE: PatentIn version 3.1
SEQ ID NO 56483
LENGTH: 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohlsen, Kari
Syskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                     Best Local Similarity 53.08
Matches 61; Conservative
NUMBER OF SEQ ID NOS: 78614
                                                                                                                       TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                             US-10-282-122A-56483
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Score 184.5; DB 15; Length 407; Pred. No. 6.4e-07;

35.5%;

Query Match Best Local Similarity

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APPLICANT: XU, H.

TITLE CONTINUATION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PELICATION NUMBER: 60/206,335
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52
                                                                                  1 AKKYAKKAEKAYAKKAKAKEKKAYAKKEAKAYK-AAEAKKKAKAEAKKYAKEA-AKAKK 58
                                                                                                                                                                                                                                                59 EAYK.-AEAKKYAKAAKAEKKEYAAAEAKK.-.-AEAAKAYKAEAAK.-.-AAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                      196 EAAKAAAEAKKKAEAEAAK----AAAEAKKKADAEAAKA-AAEAKKKADAAAAKAAAEA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAKAEAKKYAKEAAK----
17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 181.5; DB 15; Length 323;
Pred. No. 8.7e-07;
8; Mismatches 34; Indels 11;
    25; Indels
    66; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 59121, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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SEQ ID NO 59321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 52.7'
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-282-122A-59321
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PRIOR PLILING DATE: 2003-02-20
PRIOR PLILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/191,078
PRIOR PLILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-09-06
PRIOR PLILING DATE: 2000-09-06
PRIOR PLILING DATE: 2000-09-06
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-12-26
PRIOR PLILING DATE: 2001-02-66
PRIOR PLILING DATE: 2001-02-66
PRIOR PLILING DATE: 2001-02-66
PRIOR PLILING DATE: 2001-02-69
PRIOR PLILING DATE: 2001-02-66
PRIOR PLILING DATE: 2001-02-67
PRIOR PLILING DATE: 2001-02-67
PRIOR PLILING DATE: 2001-02-67
PRIOR PLILING DATE: 2001-02-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 AYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
60 AYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 347;
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49.1%; Pred. No. 1.5e-06;
tive 17; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                      Sequence 66237, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 201, Application US/10051643
; Publication No. US20020197265A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1 SEQ ID NO 66237
                                                                                                                                                                                                                                                                                                                                                                                                                                        Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen, Kari
Zyskind, Judith
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Matches 54; Conservative
                                                                                                                                                                    US-10-282-122A-66237
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US-10-051-643-201
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     Š
                                                                                                                                                         APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: ADD FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT PILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: PC1/01,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3
LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKAEKAYAKKAKAKAKEYKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Publication No. US20030113742A1

GENERAL INFORMATION

APPLICANT: Whiteley, Marvin

APPLICANT: Bangera, M. Gita

APPLICANT: Lory, Stephen

APPLICANT: Greenberg, Everett Peter

APPLICANT: Greenberg, Everett Peter

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF

TITLE OF INVENTION: BOOFILM FORMATION

FILE REFERENCE: UIZ-070CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKAEAK-----
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; Pred. No. 1.5e-06;
17; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/127,032
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,190
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: US 60/344,142
PRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PASISEQ for Windows Version 4.0
                                                    Sequence 3, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.8%;
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Best Local Similarity
Matches 54; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-10-127-032-120
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                            US-09-816-989A-3
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Search completed: December 14, 2004, 06:59:43 Job time: 271.43 secs
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           APPLICANT: Watson, James D.
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REFERENCE: 11000.1008c2
CURRENT APPLICATION NUMBER: US(10/051,643
CURRENT FILING DATE: 2002-01-18
PRIOR FILING DATE: 1996-09-17
PRIOR PLILING DATE: 1996-09-17
PRIOR PLILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 201
LENGTH: 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKK--AEKAYAKKAKAAKE---KKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKK--AEKAYAKKAKAKE---KKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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; Publication No. US20030147861A1
; GENERAL INFORMATION:
    APPLICANT: Watson, James D.
    APPLICANT: Tan, Paul L. J.
    APPLICANT: Abernethy, Nevin
    TITLE OF INVENTION: Compounds and Methods for the Modulation
    TITLE OF INVENTION: Of Immune Responses
    FILE REPERENCE: 11000.1063U
    CURRENT APPLICATION NUMBER: US/10/205,979
    CURRENT APPLICATION NUMBER: 08/10/205,979
    CURRENT PLING DATE: 2002-07-25
    PRIOR APPLICATION NUMBER: 60/308,446
    PRIOR FILING DATE: 2001-07-26
    NUMBER OF SEQ ID NOS: 52
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
34.3%; Score 178; DB 13; Length 223;
Best Local Similarity 54.5%; Pred. No. 1.1e-06;
Matches 60; Conservative 6; Mismatches 34; Indels 10
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34.3%; Score 178; DB 14; Length 223;
Best Local Similarity 54.5%; Pred. No. 1.1e-06;
Matches 60; Conservative 6; Mismatches 34; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mycobacterium vaccae US-10-051-643-201
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GENERAL INFORMATION:
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US-10-205-979-52
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RESULT 15 US-10-282-122A-75772 ; Sequence 75772, Application US/10282122A

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PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-21
PRIOR PELING DATE: 2000-05-21
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olisen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin version 3.1
SEQ ID NO 75772
LENGTH: 376
                                                                                                                                                                                                                                                  F: Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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RESULT 2
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Sequence 3, Appli
Sequence 64, Appli
Sequence 64, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 201, App
Sequence 201, App
Sequence 201, App
Sequence 3148, A
Sequence 54365, A
Sequence 64, Appli
Sequence 32, Appli
Sequence 32, Appli
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2, Appli
                                                                December 14, 2004, 05:47:53 ; Search time 30:5844 Seconds (without alignments) 236.351 Million cell updates/sec
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                                                                                                                                      1 AKKYAKKAEKAYAKKAKAAK......AKAYKAEAAKAAAKEAAYEA 109
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(GGDZ 6/ptodata/1/iaa/5A COMB.pep:*

(GGDZ 6/ptodata/1/iaa/5B COMB.pep:*

(GGDZ 6/ptodata/1/iaa/6A COMB.pep:*

(GGDZ 6/ptodata/1/iaa/6A COMB.pep:*

(GGDZ 6/ptodata/1/iaa/B COMB.pep:*

(GGDZ 6/ptodata/1/iaa/PCTUS COMB.pep:*

(GGDZ 6/ptodata/1/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-405-743A-6
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US-09-405-743A-4
US-09-405-743A-3
US-09-405-743A-3
US-09-405-743A-3
US-09-405-743A-3
US-09-405-743A-3
US-08-460-901A-64
US-08-460-901A-64
US-08-460-901A-64
US-09-252-901A-2981
US-09-270-767-3948
US-09-270-767-3948
US-09-270-767-34365
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US-09-417-264-30
US-09-417-264-30
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S-09-041-889-40
S-09-417-264-40
S-09-417-264-32
S-09-328-352-6321
S-09-328-352-5169
S-09-315-746-10
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US-09-115-746-10
US-08-216-894-2
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Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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519
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228.5
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Patent No. 651438

GENERAL INFORMATION:
TITLE OF INVENTION GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS

FILE REFERENCE: 60807-A

CURRENT APPLICATION NUMBER: US/09/405,743A

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

LENGTH: 86

TYPE: PRT

ORGANISM: Artificial Sequence
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100.0%; Score 519; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 7.1e-37;
Matches 109; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-7
                                       US-08-837-058-4

US-09-417-264-4

US-09-417-264-3

US-09-417-058-3

US-09-252-991A-32957

US-09-289-329-5

US-09-289-329-5

US-09-489-033A-13743

US-09-28-991A-22853

US-09-489-033A-13743

US-09-489-034-138-3

US-09-041-889-27

US-09-041-889-27

US-09-041-889-27

US-09-041-889-27

US-08-46-080-080-62

US-08-66-080-62
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ORGANISM: Artificial Sequence
FEATURE:
564
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2036
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158.5
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LENGTH: 56
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    SYNTHETIC
                                                                                                                                                                                                                                                          61 YKAEAKKYAKAAKAEKKEYAAAEAK-KAEAA-KAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                37 -KAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yead Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 5
SEQ ID NO 5
LENGTH: 77
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Sequence 4, Application US/09405743A

Patent No. 6514938

GENERAL INFORMATION:
APPLICANT: Yead Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A

CURRENT APPLICATION NUMBER: US/09/405,743A

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
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OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE US-09-405-743A-6
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COTHER INFORMATION: PEPTIDE
US-09-405-743A-4
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72.1%;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                    Query Match 60.2
Best Local Similarity 72.1
Matches 80; Conservative
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US-09-405-743A-5
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US-09-405-743A-4
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LENGTH: 66
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GENERAL INFORMATION:

APPLICANT:
APPLICANT:
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION:
NUCLEIC AND THERAPEUTICS

FILE REPERRUCE:
2709,2004001
CURRENT APPLICATION NUMBER: US,09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13565
                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 ADAKKQAEAAAAAKAAAEAKKQAEAEAAKAAAEAQKKAEAAAKKAQQEAEKKAQQEAAKQ 272
                                                                                                      1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
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                                                     43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLS OF INVENTION:
GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REPERBNCE:
60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE:
1999-09-24
NUMBER OF SOC ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                    1 AKKYAKK-EKAYAKAKA-----EAKAAKKA-----
                                                                                                                                                                                                     61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                    DB 4; Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 37.8*; Score 196; DB 4; Length 469
Best Local Similarity 51.2*; Pred. No. 2.9e-09;
Matches 62; Conservative 12; Mismatches 35; Indels
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 180.5; DB 4
Pred. No. 6.9e-09;
  Score 228.5; DB 4
Pred. No. 7.9e-13;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                 Sequence 13565, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 3, Application US/09405743A; Patent No. 6514938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.8%;
45.9%;
     44.0%;
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Query Match
Best Local Similarity 56.94
Matches 62; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-489-039A-13565
                                                                                                                                                                                                                                                                                                                                                    US-09-489-039A-13565
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Gaps

53;

3; Indels

3; Mismatches

50; Conservative

Matches

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Query Match 34.6%; Score 179.5; DB 3; Length 100; Best Local Similarity 55.0%; Pred. No. 1.5e-08; Matches 55; Conservative 8; Mismatches 34; Indels 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
                                                                                                      65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                               COMPOTER: IBM Compatible
COMPOTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: MARDURG, RICHARD
NAME: WARDURG, SCHARD
NAME: WARD
NAME: WARDURG, SCHARD
NAME: WARD
NAME: WARDURG, SCHARD
NAME: WARD
NA
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205/012
                                                                                                                                                                                                                                                                                                                            Sequence 64, Application US/08167641C Patent No. 6033884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               =
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 amino acids
nino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                              US-08-167-641C-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-167-641C-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
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                                                                       1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAKAEAKKYAKEAA 60
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                                                                                                                                                                                                  61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                       1 AKKYAKK-BKAYAKKA----BKAAKKABAKAYKABAKKKABAK-----
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 64, Application US/08460890A
Fatent No. 5994109
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gritiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: WIGHELC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon

K.Lyon
                                                                                                                                                                                                                                                 -----YKAEAAKAAAKEAYEA 56
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Pred. No. 1.5e-08;
8; Mismatches 34; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION 9435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/U693/02725
APPLICATION NUMBER: PCT/U693/ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32,327
RER: 212/066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 212/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
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55.0%;
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amino acid
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-460-890A-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                   40
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6 KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAE 64

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APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gridtchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FeatsEG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: Unne 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/5,389
FILING DATE: December 14, 1993
APPLICATION NUMBER: PCT/0893
APPLICATION NUMBER: PCT/0893
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/0893
ATTORNEY/AGENT INPORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                   Sequence 64, Application US/08462040
Patent No. 6177554
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   iE: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 21
IELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
STREET: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-462-040-64
                                   JS-08-462-040-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                         Sequence 44, Application US/08460971A
Patent No. 6150168
Patent No. 6150168
Patent No. 6150168
PAPLICANT: SMICH, Louis C.
APPLICANT: SMICH, Louis C.
APPLICANT: SMICH, Louis C.
APPLICANT: GOLCICAL, SEEPHEN
TITLE OF INVENTION: MCLEDIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: MCLEDIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBERS OF SEQUENCES: 6
CORRESPONDERS: 1000 K Lyon
STREET: SMICH 4700
CITY: Los Angels
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: STORED OF WINDOWS 2.0
CURRENT APPLICATION NATA: 19095
COMPUTER: IBM P.C. DOS 5.0
OPREATION SYSTEM: IBM P.C. DOS 5.0
OPREATION: 435
PRIOR TAPELICATION NATA: 19093
APPLICATION NUMBER: 07/0855, 1995
CLASSIFICATION NUMBER: 07/0855, 1995
APPLICATION NUMBER: 07/0855, 1995
APPLICATION NUMBER: 20.71093
APPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.6%; Score 179.5; DB 3; Length 100; Best Local Similarity 55.0%; Pred. No. 1.5e-08; Matches 55; Conservative 8; Mismatches 34; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                      RESULT 9
US-08-460-971A-64
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6 KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKKEAYKAE . M Length 100; ch 34.6%; Score 179.5; DB 3; Length Il Similarity 55.0%; Pred. No. 1.5e-08; 55; Conservative 8; Mismatches 34; Indels 65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103 60 акакакакакакакакакакакакакакакакакак RESULT 11 US-09-252-991A-29581 ; Sequence 29581, Application US/09252991A

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Sequence 5390, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKK--AEKAYAKKAKAKAKE---KKAYAKKEAKAYKAAEAKKKAKAKAKAKAAK 55
                                                                                                                                                                                                                                                                                                                                                                                       Score 178; DB 3; Length 223;
Pred. No. 4.4e-08;
6; Mismatches 34; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Watson, James D.
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
FILE REFERENCE: 11000.11002.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.3%; Score 178; DB 4; Length 22:
54.5%; Pred. No. 4.4e-08;
iive 6; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 1998-12-04

CURRENT FILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: 09/095,855

EARLIER APPLICATION NUMBER: 09/997,362

EARLIER FILING DATE: 1998-06-11

EARLIER FILING DATE: 1997-12-23

EARLIER FILING DATE: 1997-12-23

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1996-08-29

NUMBER OF SEQ ID NOS: 208

SOFTWARE: FASCED for Windows Version 3.0

SEQ ID NO 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 201, Application US/09205426
Patent No. 6406704
GENERAL INFORMATION:
                                                                  201:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-205-426-201
           INFORMATION FOR SEQ ID NO: 201
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids

"The control of the control o
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1 Similarity 54.5%;
60; Conservative 6
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Matches 60; Conservative
TELEFAX: 206-269-0563
                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-095-855-201
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 60; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-543-681A-5390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-205-426-201
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                      GENERAL INCORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 201, Application US/09095855
Patent No. 6160093
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Stinner, Margot
APPLICANT: Stinner, Margot
APPLICANT: Stinner, Margot
APPLICANT: Stinner, Margot
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 KKAEKAYAKKAKAAKEK-----KAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 AYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.5%; Score 179; DB 4; Length 407; 49.1%; Pred. No. 6.7e-08; tive 17; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FSELSEG for Windows Version 2.0
CURTENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sleath, Janet
REGISTRATION WUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/97,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 49.1..
Local Similarity 49.1..
S4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-095-855-201
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1 AKKYAKKAEKAYAKKAKAKAKAYAKKEAKAYKA-----AEAKKKAKAEAKKYAK 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-09-270-767-39148
US-09-270-767-39148
Sequence 39148, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburse et al.
TITLE OF INVENTION: Widele acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 39148
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 32.6%; Score 169; DB 4; Length 361;
Best Local Similarity 44.0%; Pred. No. 4e-07;
Matches 51; Conservative 16; Mismatches 37; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.6%; Score 164; DB 4; Length 171; 42.9%; Pred. No. 5e-07; tive 20; Mismatches 30; Indels ;
             CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
LENGTH: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Drosophila melanogaster US-09-270-767-39148
FILE REFERENCE: 2709.1002-001
                                                                                                                                                                    TYPE: PRT
ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 42.9*
Matches 57; Conservative
                                                                                                                                                                                                                 US-09-543-681A-5390
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48 KYAKEAA-----KAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKA--E 96
                                                  97 AAKAAAKEAAYEA 109
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141 AAQKAAEEAALKA 153
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Search completed: December 14, 2004, 05:50:19 Job time : 31.7272 secs